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OM protein - protein search, using sw model

Run on: October 1, 2004, 20:50:35 ; Search time 128 Seconds

(without alignments)
869.717 Million cell updates/sec

Title: US-09-989-728-422

Perfect score: 2067

Sequence: 1 MFCLPLKILFLVLLSYSLG.....RNSLSKSGGMPKTOQAP 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2067	100.0	394	3 AAY66764	Aay66764 Membrane-
2	2067	100.0	394	3 AAB33454	Aab33454 Human PRO
3	2067	100.0	394	3 AAY94452	Aay94452 Human inf
4	2067	100.0	394	3 AAB24433	Aab24433 Human PRO
5	2067	100.0	394	4 AAU12431	Aau12431 Human PRO
6	2067	100.0	394	4 AAM38860	Aam38860 Human pol
7	2067	100.0	394	4 AAB65287	Aab65287 Human PRO
8	2067	100.0	394	5 AAU83689	Aau83689 Human PRO
9	2067	100.0	394	5 ABB84933	Abb84933 Human PRO
10	2067	100.0	394	5 ABB95539	Abb95539 Human ang
11	2067	100.0	394	6 ABUS8102	Abus8102 Human PRO
12	2067	100.0	394	6 ABUS9180	Abus9180 Novel hum
13	2067	100.0	394	6 ABUS9262	Abus9262 Human sec
14	2067	100.0	394	6 ABO17875	Abo17875 Novel hum
15	2067	100.0	394	6 ABUS6061	Abus6061 Human sec
16	2067	100.0	394	6 ABUS0836	Abus0836 Human PRO
17	2067	100.0	394	6 ABO33802	Abo33802 Novel hum
18	2067	100.0	394	6 ABUI3993	Abui3993 Human PRO
19	2067	100.0	394	6 ABUS1129	Abus1129 Human PRO
20	2067	100.0	394	6 ABUT2578	Abut2578 Novel hum
21	2067	100.0	394	6 ABUS6829	Abus6829 Human PRO
22	2067	100.0	394	6 ABUS5910	Abus5910 Novel sec
23	2067	100.0	394	6 ABUS9327	Abus9327 Human sec
24	2067	100.0	394	6 ABO26024	Abo26024 Human PRO
25	2067	100.0	394	6 ABO25100	Abo25100 Human sec

26	2067	100.0	394	6 ABUS2145	Abu82145 Novel hum
27	2067	100.0	394	6 ABUS9033	Abu59033 Human sec
28	2067	100.0	394	6 ABUS2411	Abu92411 Novel hum
29	2067	100.0	394	6 ABUS9476	Abu59476 Novel hum
30	2067	100.0	394	6 ABUS7105	Abu67105 Human sec
31	2067	100.0	394	6 ABUS2242	Abu92242 Novel hum
32	2067	100.0	394	6 ABUI0948	Abui0948 Human PRO
33	2067	100.0	394	6 ABUS1700	Abu81700 Novel hum
34	2067	100.0	394	6 ABUS8639	Abu88639 Human sec
35	2067	100.0	394	6 ABO34153	Abo34153 Human PRO
36	2067	100.0	394	6 ADA46039	Ada46039 Novel hum
37	2067	100.0	394	6 ADA76470	Ada76470 Human PRO
38	2067	100.0	394	6 ABJ72325	Abj72325 Human PRO
39	2067	100.0	394	6 ADA19120	Ada19120 Human PRO
40	2067	100.0	394	6 ADA61743	Ada61743 Homo sapi
41	2067	100.0	394	6 ADB19528	Adb19528 Novel hum
42	2067	100.0	394	6 ADB28069	Adb28069 Human PRO
43	2067	100.0	394	6 ADA86548	Ada86548 Novel hum
44	2067	100.0	394	6 ADB16112	Adb16112 Human PRO
45	2067	100.0	394	6 ADA37933	Ada37933 Human sec

ALIGNMENTS

RESULT 1

AAY66764

ID AAY66764 standard; protein; 394 AA.

XX AC AAY66764;

XX XX

DI 05-APR-2000 (first entry)

XX XX

DE DE Membrane-bound protein PRO1387.

XX XX

KW KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping.

XX OS Homo sapiens.

XX XX

PN WO9963088-A2.

XX XX

PD 09-DEC-1999.

XX XX

PF 02-JUN-1999; 93WO-US012252.

XX XX

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088326P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088722P.

PR 10-JUN-1998; 98US-0088730P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088740P.

PR 10-JUN-1998; 98US-0088742P.

PR 10-JUN-1998; 98US-0088745P.

PR 10-JUN-1998; 98US-0088810P.

PR 10-JUN-1998; 98US-0088811P.

PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088825P.

Db 61 PGEHAKDEVLYYYNSLSPVPIGRFQNRVHLMGDI LNDGSLLLQDVQVQADQGTTCIEIRL 120
QY 121 KGESQVFKKAVVHLVLPPEPKELMVHVGGI LQMGCVFQSTEVKHVTKVEMIFSGRAKEE 180
Db 121 KGESQVFKKAVVHLVLPPEPKELMVHVGGI LQMGCVFQSTEVKHVTKVEMIFSGRAKEE 180
QY 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGD IFRNDGSI MLQGVRESGDNVTCSTHILGN 240
Db 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGD IFRNDGSI MLQGVRESGDNVTCSTHILGN 240
QY 241 LVFKKTIIVLHVSPEEPRTLTPAALRPLV LGGNQLVIIGVIVCATILLPVLLIVKKT 300
Db 241 LVFKKTIIVLHVSPEEPRTLTPAALRPLV LGGNQLVIIGVIVCATILLPVLLIVKKT 300
QY 301 GNKSSVNSTVLVKNTKTNPEIKPKCHPFCRCEGEKHIIYSP IIVREVIEEPPSEKSEAT 360
Db 301 GNKSSVNSTVLVKNTKTNPEIKPKCHPFCRCEGEKHIIYSP IIVREVIEEPPSEKSEAT 360
QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTKQOAF 394
Db 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTKQOAF 394

RESULT 3
AA94452
ID AA94452 standard; protein; 394 AA.
AC AA94452;
DT 11-SEP-2000 (first entry)
XX Human inflammation associated protein #11.
DE Inflammation; rheumatoid arthritis; Crohn's disease; asthma;
KW multiple sclerosis; allergy; AIDS; diabetes mellitus antiinflammatory;
KW gene therapy; human.
OS Homo sapiens.
XX WO200029574-A2.
PN 25-MAY-2000.
XX 04-NOV-1999; 99WO-US026234.
XX 18-NOV-1998; 98US-00195292.
XX (INCY-) INCYTE PHARM INC.
PA Walker MG, Volkmut W, Klingler TM;
PI WPI; 2000-387787/33.
XX N-PSDB; AAA27133.

XX New human inflammation-associated polypeptide useful for diagnosis,
PT prevention and treatment of inflammatory diseases comprises product of
PT Gene coexpressed with e.g. CD16, L-selectin and IP-30.
XX Claim 4; Page 42-43; 43pp; English.
XX Eleven novel inflammation-associated genes have been identified in cDNA
CC libraries from various tissues. The genes were selected according to
CC their coexpression with the known inflammation genes, CD16, L-selectin,
CC Src-like adapter protein, IP-30, superoxide homocysteine subunits, alpha-
CC l-antitrypsin, C1q-A, 5-lipoxygenase activating protein and SRC family
CC tyrosine kinase. The novel polynucleotides may be used in hybridization
CC assays to diagnose a disease or condition associated with altered
CC expression of the inflammation genes. Antibodies against the genes may be
CC useful in compositions for the diagnosis and treatment of such diseases
CC associated with inflammation including rheumatoid arthritis, Crohn's
CC disease, multiple sclerosis, AIDS, diabetes mellitus, asthma and allergy.
CC Additionally the polynucleotides of the invention may be used for gene
CC therapy. The present sequence is human inflammation associated protein

CC #11, derived from Incyte Clone 3507924
XX Sequence 394 AA;
QY Query Match 100.0%; Score 2067; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKILLPVLLDYSIGLNDLVNVPPELT VHVGDLSALMGCVFQSTEDKCFKIDWTLS 60
Db 1 MFCPLKILLPVLLDYSIGLNDLVNVPPELT VHVGDLSALMGCVFQSTEDKCFKIDWTLS 60
QY 61 PGEHAKDEVLYYYNSLSPVPIGRFQNRVHLMGDI LNDGSLLLQDVQVQADQGTTCIEIRL 120
Db 61 PGEHAKDEVLYYYNSLSPVPIGRFQNRVHLMGDI LNDGSLLLQDVQVQADQGTTCIEIRL 120
QY 121 KGESQVFKKAVVHLVLPPEPKELMVHVGGI LQMGCVFQSTEVKHVTKVEMIFSGRAKEE 180
Db 121 KGESQVFKKAVVHLVLPPEPKELMVHVGGI LQMGCVFQSTEVKHVTKVEMIFSGRAKEE 180
QY 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGD IFRNDGSI MLQGVRESGDNVTCSTHILGN 240
Db 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGD IFRNDGSI MLQGVRESGDNVTCSTHILGN 240
QY 241 LVFKKTIIVLHVSPEEPRTLTPAALRPLV LGGNQLVIIGVIVCATILLPVLLIVKKT 300
Db 241 LVFKKTIIVLHVSPEEPRTLTPAALRPLV LGGNQLVIIGVIVCATILLPVLLIVKKT 300
QY 301 GNKSSVNSTVLVKNTKTNPEIKPKCHPFCRCEGEKHIIYSP IIVREVIEEPPSEKSEAT 360
Db 301 GNKSSVNSTVLVKNTKTNPEIKPKCHPFCRCEGEKHIIYSP IIVREVIEEPPSEKSEAT 360
QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTKQOAF 394
Db 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTKQOAF 394

RESULT 4
AAB24433
ID AAB24433 standard; protein; 394 AA.
XX AAB24433;
DT 07-NOV-2000 (first entry)
XX Human PRO1387 protein sequence SEQ ID NO:220.
DE Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW cytotatic; gene therapy; vaccine.
XX Homo sapiens.
XX WO200032221-A2.
XX 08-JUN-2000.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 12-JAN-1999; 99US-0115554P.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 25-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.

AAU12431 standard; protein; 394 AA.
 AAU12431;
 24-OCT-2001 (first entry)
 Human PRO1387 polypeptide sequence.
 Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 A-peptide; factor VIIA; gene therapy.
 Homo sapiens.
 WO200140466-A2.
 07-JUN-2001.
 01-DEC-2000; 2000WO-US032678.
 01-DEC-1999; 99WO-US028301.
 01-DEC-1999; 99WO-US028634.
 02-DEC-1999; 99WO-US028551.
 02-DEC-1999; 99WO-US028564.
 02-DEC-1999; 99WO-US028565.
 09-DEC-1999; 99US-0170262P.
 16-DEC-1999; 99WO-US030095.
 20-DEC-1999; 99WO-US030911.
 20-DEC-1999; 99WO-US030999.
 30-DEC-1999; 99WO-US031243.
 30-DEC-1999; 99WO-US031274.
 05-JAN-2000; 2000WO-US000219.
 06-JAN-2000; 2000WO-US000277.
 06-JAN-2000; 2000WO-US000376.
 11-FEB-2000; 2000WO-US003565.
 18-FEB-2000; 2000WO-US004341.
 18-FEB-2000; 2000WO-US004342.
 22-FEB-2000; 2000WO-US004414.
 24-FEB-2000; 2000WO-US004914.
 24-FEB-2000; 2000WO-US005004.
 02-MAR-2000; 2000WO-US005601.
 02-MAR-2000; 2000WO-US005841.
 10-MAR-2000; 2000US-0187202P.
 15-MAR-2000; 2000WO-US00684.
 20-MAR-2000; 2000WO-US007377.
 21-MAR-2000; 2000WO-US007532.
 30-MAR-2000; 2000WO-US008439.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 05-JUN-2000; 2000US-0209832P.
 28-JUL-2000; 2000WO-US020710.
 11-AUG-2000; 2000WO-US022031.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 08-NOV-2000; 2000WO-US030952.
 10-NOV-2000; 2000WO-US030873.
 (GETH) GENENTECH INC.
 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 WPI; 2001-408281/43.
 N-PSDB; AAG21503.
 Isolated , secretory and transmembrane PRO polypeptide used to detect
 other PRO polypeptides, link bioactive molecules to cells expressing PRO
 polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT

13-SEP-1999; 99WO-US020944.
 15-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021547.
 05-OCT-1999; 99WO-US023089.
 29-OCT-1999; 99US-0162506P.
 (GETH) GENENTECH INC.
 Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
 PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
 PI Smith V, Watanabe CK, Williams PM, Wood WI;
 WPI; 2000-412154/35.
 N-PSDB; AAA77683.
 Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
 and treating diagnosing a cardiovascular, endothelial or angiogenic
 disorders in mammals.
 Claim 72; Fig 92; 315pp; English.
 The present invention describes nucleic acids encoding PRO polypeptides
 useful for preventing, diagnosing and treating diagnosing a
 cardiovascular, endothelial or angiogenic disorder in mammals by
 modulating cell proliferation, angiogenesis and cardiovascularisation,
 and for identifying agonists and antagonists of these processes. The
 nucleic acids and the proteins they encode may be used in the prevention,
 treatment and diagnosis of diseases associated with inappropriate PRO
 expression such as cardiovascular, cancers and vectors containing them and the PRO
 mammals (e.g. atherosclerosis, cancers and vectors containing them and the PRO
 polypeptide may be used to treat disorders associated with decreased PRO
 expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
 nucleotide and protein sequences used in the exemplification of the
 present invention
 Sequence 394 AA;
 Query Match 100.0%; Score 2067; DB 3; Length 394;
 Best Local Similarity 100.0%; Pred. No. 5.1e-188;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFCEKLKLLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
 Db 1 MFCEKLKLLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
 QY 61 PGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDIKNDGSLLOVQADQGTVCIEIRL 120
 Db 61 PGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDIKNDGSLLOVQADQGTVCIEIRL 120
 QY 121 KGESQVFKAIVHLVPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEMIFSGRRAKEE 180
 Db 121 KGESQVFKAIVHLVPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEMIFSGRRAKEE 180
 QY 181 IVFRIYHKLRSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHLGN 240
 Db 181 IVFRIYHKLRSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHLGN 240
 QY 241 LVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGNQLVIVGIVCATILLPVLILVKKTC 300
 Db 241 LVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGNQLVIVGIVCATILLPVLILVKKTC 300
 QY 301 GNKSSVNSVTLVKNKTTPKEIKPCHPERCEGEKHIYSPPIVREVEEPEPSEKSEAT 360
 Db 301 GNKSSVNSVTLVKNKTTPKEIKPCHPERCEGEKHIYSPPIVREVEEPEPSEKSEAT 360
 QY 361 YMTMHPVWPSLRDRNNSLEKSGGMPKTTQQAF 394
 Db 361 YMTMHPVWPSLRDRNNSLEKSGGMPKTTQQAF 394
 RESULT 5
 AAU12431

PT breast, prostate, cervical.

Claim 12; Fig 520; 813pp; English.

AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIa. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy

Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCPLKLLPVLIDYSLGNDLNVSPPELTQVHVGDSALMGCVFQSTEDKCFIKIDWTLS 60
DB 1 MFCPLKLLPVLIDYSLGNDLNVSPPELTQVHVGDSALMGCVFQSTEDKCFIKIDWTLS 60
QY 61 PGEHAKDEYVLYYSNLSVPFGRFQNRVHLMGDIICNDGSLLLQDVQADQGYICEIRL 120
DB 61 PGEHAKDEYVLYYSNLSVPFGRFQNRVHLMGDIICNDGSLLLQDVQADQGYICEIRL 120
QY 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRAKEE 180
DB 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRAKEE 180
QY 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESDGNYTCSHLGN 240
DB 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESDGNYTCSHLGN 240
QY 241 LVFKKTIHLVHSPPEPRTLVTFAALRPLVLGNGQLVLIIGVIVCATILLPVLILIVKKT 300
DB 241 LVFKKTIHLVHSPPEPRTLVTFAALRPLVLGNGQLVLIIGVIVCATILLPVLILIVKKT 300
QY 301 GNKGSVNSTVLVKNTKTNPEIKPKCHPERCEGKEKHIYSPPIVREVIEEPEPSEKSEAT 360
DB 301 GNKGSVNSTVLVKNTKTNPEIKPKCHPERCEGKEKHIYSPPIVREVIEEPEPSEKSEAT 360
QY 361 YMTMHPVWPSLRDRNNSLEKSGGMPKTOQAF 394
DB 361 YMTMHPVWPSLRDRNNSLEKSGGMPKTOQAF 394

RESULT 6

AAU38860
ID AAU38860 standard; protein; 394 AA.

XX AAU38860;

AC 22-OCT-2001 (first entry)

DT Human polypeptide SEQ ID NO 2005.

DE Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;

XX peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW

anyotropic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

PN 26-JUL-2001.

PD 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 98US-00471275.

XX 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AAI58016.

XX Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

XX Example 3; SEQ ID NO 2005; 10078pp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAU38642-AAU42213) with nontropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral neuropathies, peripheral neuropathy and localized neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

XX Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCPLKLLPVLIDYSLGNDLNVSPPELTQVHVGDSALMGCVFQSTEDKCFIKIDWTLS 60
DB 1 MFCPLKLLPVLIDYSLGNDLNVSPPELTQVHVGDSALMGCVFQSTEDKCFIKIDWTLS 60
QY 61 PGEHAKDEYVLYYSNLSVPFGRFQNRVHLMGDIICNDGSLLLQDVQADQGYICEIRL 120
DB 61 PGEHAKDEYVLYYSNLSVPFGRFQNRVHLMGDIICNDGSLLLQDVQADQGYICEIRL 120
QY 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRAKEE 180
DB 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRAKEE 180
QY 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESDGNYTCSHLGN 240
DB 181 IVFRYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESDGNYTCSHLGN 240

PT	molecules such as toxins, radiolabels or antibodies, to specific cells,		
PI	to cause targeted cell death.		
XX	Claim 12; Fig 304; 935pp; English.		
XX	The present invention describes human secreted and transmembrane PRO		
CC	proteins. The PRO proteins have cytostatic activity. The PRO proteins can		
CC	be used for targeted delivery of bioactive molecules, such as toxins,		
CC	radiolabels or antibodies, that cause cell death. PRO nucleotide		
CC	sequences, and their fragments, can be used as hybridisation probes, in		
CC	chromosomal and gene mapping, and in the generation of anti-sense RNA and		
CC	DNA. They may also be used to produce transgenic animals which are used		
CC	to develop and screen therapeutically useful reagents. The PRO nucleotide		
CC	and protein sequence can be used for tissue typing and in treating		
CC	cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to		
CC	AAF44470 represent PCR primers and hybridisation probes used in the		
CC	isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to		
CC	AAB65300 represent human PRO polynucleotide and protein sequences given		
CC	in the exemplification of the present invention		
XX	Sequence 394 AA;		
SQ			
Query Match		100.0%; Score 2067; DB 4; Length 394;	
Best Local Similarity		100.0%; Pred. No. 5.1e-188;	
Matches 394; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MFCPLKLIILLPVLLDYSGLNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIKIDWTLS	60
Db	1	MFCPLKLIILLPVLLDYSGLNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIKIDWTLS	60
QY	61	PGEHAKDEVLYYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGTIYCEIRL	120
Db	61	PGEHAKDEVLYYYNSLVPIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGTIYCEIRL	120
QY	121	KGESQVFKKAVLHLVLPPEPKELMWHVGGIOMGCVFQSTEVKHVTKVEMIFSGRAKEE	180
Db	121	KGESQVFKKAVLHLVLPPEPKELMWHVGGIOMGCVFQSTEVKHVTKVEMIFSGRAKEE	180
QY	181	IVFRYHYHKLMSVEYSQSWGHFNQNRVNLVGDIFRNDGSLMLQGVRESGDNYSIHGLN	240
Db	181	IVFRYHYHKLMSVEYSQSWGHFNQNRVNLVGDIFRNDGSLMLQGVRESGDNYSIHGLN	240
QY	241	LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGGNQLVVIIVGIVCATILLPVLILIVKTC	300
Db	241	LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGGNQLVVIIVGIVCATILLPVLILIVKTC	300
QY	301	GNKSSVNSTVLVNTKTNPEIKPKCHPERCEGKHIYSPIIIVREVEEPEPSEKSEAT	360
Db	301	GNKSSVNSTVLVNTKTNPEIKPKCHPERCEGKHIYSPIIIVREVEEPEPSEKSEAT	360
QY	361	YMTMHPVWPSLRSDRNNLSLEKSGGMPKTKQAF	394
Db	361	YMTMHPVWPSLRSDRNNLSLEKSGGMPKTKQAF	394
RESULT 8			
AAU83689	ID	AAU83689 standard; protein; 394 AA.	
XX	AC	AAU83689;	
XX	DT	08-MAY-2002 (first entry)	
XX	DE	Human PRO protein, Seq ID No 196.	
XX	XX	Human; secreted protein; PRO; tumour; lung cancer; colon cancer;	
KW	KW	breast cancer; prostate tumour; rectal tumour; liver tumour;	
KW	KW	pericyte cell proliferation; chondrocyte cell proliferation;	
KW	KW	tumour necrosis factor-alpha.	
XX	OS	Homo sapiens.	
XX	XX	WO200208288-A2.	

XX PD 31-JAN-2002.
 XX PF 29-JUN-2001; 2001WO-US021066.
 XX PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220585P.
 PR 25-JUL-2000; 2000US-0220605P.
 PR 25-JUL-2000; 2000US-0220607P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220638P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 25-JUL-2000; 2000US-0220666P.
 PR 26-JUL-2000; 2000US-0220893P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 01-AUG-2000; 2000US-0222425P.
 PR 02-AUG-2000; 2000US-0227133P.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 28-NOV-2000; 2000US-0253646P.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001WO-US017092.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX N-PSDB; ABK33633.
 DR MPI; 2002-172001/22.
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumors such
 PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
 PT or liver tumor.
 XX Claim 11; Fig 196; 359pp; English.
 XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumors, especially lung
 CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
 CC liver tumor. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention
 XX Sequence 394 AA;
 SQ
 Query Match 100.0%; Score 2067; DB 5; Length 394;
 Best Local Similarity 100.0%; Pred. No. 5.1e-188;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFCPLKILLPVLVDYSIGLNDLNVPPELTVHVGDSALMGCVFQSTEDKCFIKIDWTLS 60
 DB 1 MFCPLKILLPVLVDYSIGLNDLNVPPELTVHVGDSALMGCVFQSTEDKCFIKIDWTLS 60

QY 61 PGEHAKDEYLVLYYNSNLSPVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGTTCIEIRL 120
 DB 61 PGEHAKDEYLVLYYNSNLSPVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGTTCIEIRL 120
 QY 121 KGESQVFKKAVLVHLVPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWEIFSGRAKEE 180
 DB 121 KGESQVFKKAVLVHLVPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWEIFSGRAKEE 180
 QY 181 IVFRYYHKLMSVEYSQSMGHFQNRVNLVGDIFRNDGSIIMLGQVRESGDNVTCSHLGN 240
 DB 181 IVFRYYHKLMSVEYSQSMGHFQNRVNLVGDIFRNDGSIIMLGQVRESGDNVTCSHLGN 240
 QY 241 LVFKKTIIVLHVSPEEPRTLVTTPAALRPLVGLGNQLVIVGIVCATILLPVLILVKKTC 300
 DB 241 LVFKKTIIVLHVSPEEPRTLVTTPAALRPLVGLGNQLVIVGIVCATILLPVLILVKKTC 300
 QY 301 GNKSSVNSTVLVQNTKTNPKIKPKCHPERCEGEKHIYSPILVREVIEEPEPSKSEAT 360
 DB 301 GNKSSVNSTVLVQNTKTNPKIKPKCHPERCEGEKHIYSPILVREVIEEPEPSKSEAT 360
 QY 361 YMTMHPVWPSLRSRDRNNSLEKSGGMPKTOQAF 394
 DB 361 YMTMHPVWPSLRSRDRNNSLEKSGGMPKTOQAF 394
 RESULT 9
 ABB84933
 ID ABB84933 standard; protein; 394 AA.
 XX AC ABB84933;
 XX DT 16-MAY-2002 (first entry)
 XX Human PRO1387 protein sequence SEQ ID NO:234.
 DE Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX Homo sapiens.
 OS
 XX WO200200690-A2.
 PN
 XX 03-JAN-2002.
 PD
 XX 20-JUN-2001; 2001WO-US019692.
 XX 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.

28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
09-MAR-2001; 2001US-00802706.
14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-00828366.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001US-00866034.
30-MAY-2001; 2001US-00870574.
30-MAY-2001; 2001US-00870574.
01-JUN-2001; 2001WO-US017800.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI; 2002-090516/12.
DR N-PSDB; ABL88188.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 11; Fig 234; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,
CC antiangiogenic, hypotensive, vulnary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
XX Sequence 394 AA;
SQ
Query Match 100.0%; Score 2067; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFCPLKLLPVLDDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Db 1 MFCPLKLLPVLDDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
Qy 61 PGEHAKDEYLVYYNSLVSPVIGRQNRVHLMGDIICNDGSLLLQDVQADQGTVCIEIRL 120
Db 61 PGEHAKDEYLVYYNSLVSPVIGRQNRVHLMGDIICNDGSLLLQDVQADQGTVCIEIRL 120
Qy 121 KGESQVFKKAVLVHVLPEEPKELMVHVGGLIQMGCVFQSTEDKCFKIDWTLS 180
Db 121 KGESQVFKKAVLVHVLPEEPKELMVHVGGLIQMGCVFQSTEDKCFKIDWTLS 180
Qy 181 IVFRYHKLRLMSVEYSQSWGHFQNRVNLVIGDIFRNDGSLIMLQGVRESQDGNVTCISHLGN 240
Db 181 IVFRYHKLRLMSVEYSQSWGHFQNRVNLVIGDIFRNDGSLIMLQGVRESQDGNVTCISHLGN 240
Qy 241 LVFKKTIIVHVSPEPRTLVTAAALPLVIGNQNLVIVGIVCATILLPVLIVKTC 300
Db 241 LVFKKTIIVHVSPEPRTLVTAAALPLVIGNQNLVIVGIVCATILLPVLIVKTC 300
Qy 301 GNKSSVNSTVLVNTKTNPEIKPCHPERCEGKHIYSPITVREVIEEPEPSEKSEAT 360

Db 301 GNKSSVNSTVLVNTKTNPEIKPCHPERCEGKHIYSPITVREVIEEPEPSEKSEAT 360
Qy 361 YNTMHPVWPSLRSDRNNLSLEKSGGGMPTQOAF 394
Db 361 YNTMHPVWPSLRSDRNNLSLEKSGGGMPTQOAF 394
RESULT 10
ABB95539
ID ABB95539 standard; protein; 394 AA.
XX
AC ABB95539;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO1387 SEQ ID NO: 234.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnary;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021735.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-0222695P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
XX (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PW, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-ESDB; ABL95677.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
PS Claim 11; Fig 234; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCPLKLILPVLVDYSLGNDLNVSPPELTIVHVDGSLMGCVFQSTEDKCFKIDWTL 60
Db 1 MFCPLKLILPVLVDYSLGNDLNVSPPELTIVHVDGSLMGCVFQSTEDKCFKIDWTL 60
QY 61 PGBHAKDEVLYYXSNLSVPIGRFQNRVHLMGDI LNDGSLLLQDVQEAQGYVCIRL 120
Db 61 PGBHAKDEVLYYXSNLSVPIGRFQNRVHLMGDI LNDGSLLLQDVQEAQGYVCIRL 120
QY 121 KGESQVFKKAVLHVLPEEPKELMHVGGI LMGCVFQSTEVKHVTKVEMIFSGRAKEE 180
Db 121 KGESQVFKKAVLHVLPEEPKELMHVGGI LMGCVFQSTEVKHVTKVEMIFSGRAKEE 180
QY 181 IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSI LMGVRESDGNYTCSHLGN 240
Db 181 IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSI LMGVRESDGNYTCSHLGN 240
QY 241 LVFKTIVLHVSPPEERTLVTPAALPLVLGGNQLVIIGVICATILLPVLILVKKTC 300
Db 241 LVFKTIVLHVSPPEERTLVTPAALPLVLGGNQLVIIGVICATILLPVLILVKKTC 300
QY 301 GNKSSVNSTVLVKNTKTNPEIKKCHPERCEGKHYSPIIVREVEEBEPESEKSEAT 360
Db 301 GNKSSVNSTVLVKNTKTNPEIKKCHPERCEGKHYSPIIVREVEEBEPESEKSEAT 360
QY 361 YNTMHPVWPSLSDRNNLSLEKSGGGMPTQQAF 394
Db 361 YNTMHPVWPSLSDRNNLSLEKSGGGMPTQQAF 394

RESULT 11
ABUS8102
ID ABUS8102 standard; protein; 394 AA.
XX
AC ABUS8102;
XX

DT 14-APR-2003 (first entry)
XX
DE Human PRO polypeptide #134.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
XX antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0085311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088555P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089601P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 23-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.

PR	23-JUN-1998;	98US-0090355P.	PR	26-AUG-1998;	98US-0098014P.
PR	24-JUN-1998;	98US-0090429P.	PR	31-AUG-1998;	98US-0098525P.
PR	24-JUN-1998;	98US-0090431P.	PR	16-SEP-1998;	98US-0100634P.
PR	24-JUN-1998;	98US-0090435P.	PR	16-SEP-1998;	98WO-US019330.
PR	24-JUN-1998;	98US-0090444P.	PR	17-SEP-1998;	98US-0100858P.
PR	24-JUN-1998;	98US-0090445P.	PR	17-SEP-1998;	98WO-US019437.
PR	24-JUN-1998;	98US-0090472P.	PR	07-OCT-1998;	98WO-US021141.
PR	24-JUN-1998;	98US-0090535P.	PR	01-DEC-1998;	98WO-US025108.
PR	24-JUN-1998;	98US-0090540P.	PR	22-DEC-1998;	98US-0113298P.
PR	24-JUN-1998;	98US-0090542P.	PR	05-JAN-1999;	99WO-US000106.
PR	24-JUN-1998;	98US-0090557P.	PR	08-MAR-1999;	99WO-US005028.
PR	25-JUN-1998;	98US-0090676P.	PR	12-MAR-1999;	99US-0123957P.
PR	25-JUN-1998;	98US-0090678P.	PR	02-JUN-1999;	99WO-US012252.
PR	25-JUN-1998;	98US-0090690P.	PR	23-JUN-1999;	99US-0141037P.
PR	25-JUN-1998;	98US-0090695P.	PR	07-JUL-1999;	99US-0143048P.
PR	25-JUN-1998;	98US-0090696P.	PR	20-JUL-1999;	99US-0144758P.
PR	25-JUN-1998;	98US-0090696P.	PR	26-JUL-1999;	99US-0145698P.
PR	26-JUN-1998;	98US-0090862P.	PR	28-JUL-1999;	99US-0146222P.
PR	26-JUN-1998;	98US-0090863P.	PR	17-AUG-1999;	99US-0149396P.
PR	01-JUL-1998;	98US-0091360P.	PR	15-SEP-1999;	99WO-US021090.
PR	02-JUL-1998;	98US-0091478P.	PR	15-SEP-1999;	99WO-US021547.
PR	02-JUL-1998;	98US-0091519P.	PR	08-OCT-1999;	99US-0158663P.
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Db	1	MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDLSALMGCVFQSTEDKCIFKIDWTLS	60	1	MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDLSALMGCVFQSTEDKCIFKIDWTLS
Qy	61	PGEHAKDEYVLYYYNSLVPIGRFQNRVHLMGDIKNDGSLLLQDVQADQGTVICEIRL	120	61	PGEHAKDEYVLYYYNSLVPIGRFQNRVHLMGDIKNDGSLLLQDVQADQGTVICEIRL
Db	61	PGEHAKDEYVLYYYNSLVPIGRFQNRVHLMGDIKNDGSLLLQDVQADQGTVICEIRL	120	61	PGEHAKDEYVLYYYNSLVPIGRFQNRVHLMGDIKNDGSLLLQDVQADQGTVICEIRL
Qy	121	KGESQVFKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKEVTFSGRRAKEE	180	121	KGESQVFKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKEVTFSGRRAKEE
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Qy	181	IVFRYHKLRLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLIMLQGVRESGGNYTCSIHGN	240	181	IVFRYHKLRLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLIMLQGVRESGGNYTCSIHGN
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Qy	241	LVFKKTIYLVHVSPEEPRTLVTPAALRPLVLGGNQLVIVGIVCATILLPVLILVKKTC	300	241	LVFKKTIYLVHVSPEEPRTLVTPAALRPLVLGGNQLVIVGIVCATILLPVLILVKKTC

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RESULT 12
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 DT 28-APR-2003 (first entry)
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 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disease;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.
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 OS Homo sapiens.
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 PN US2002132252-A1.
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 PD 19-SEP-2002.
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 PF 14-NOV-2001; 2001US-00990442.
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 PR 07-OCT-1998; 98WO-US021141.
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 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
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 PR 09-JUL-2001; 2001WO-US021735.
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 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 XX WPI: 2003-247083/24.
 DR N-PSDB; ABX80392.
 XX
 XX Novel isolated PRO polypeptides e.g., PRO826, PRO1184, PRO1346

PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX Claim 12; Fig 304; 648pp; English.
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO336,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
XX amino acid sequence of a novel human PRO protein

SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
ABU82692

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AC ABU82692;
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XX 26-JUN-2003 (first entry)
XX Human secreted/transmembrane protein PRO1387.
DE
XX Human; PRO; secreted protein; transmembrane protein; wound healing;
XX cardiac insufficiency disorders; angiogenesis; wound healing;
XX cancerous tumour; immune response; retinal disorder; sight loss;
XX retinitis pigmentosa; age-related macular degeneration; AMD;
XX kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
XX Crohn's disease; sports injury; arthritis.
XX Homo sapiens.
OS
XX US2003032023-A1.
PN
XX 13-FEB-2003.
PD
XX 14-NOV-2001; 2001US-00990711.
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PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US0003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 02-MAR-2000; 2000WO-US005004.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US007377.
PR 15-MAY-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013358.
PR 22-MAY-2000; 2000WO-US013705.
PR 30-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US014941.
PR 23-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000US-0213637P.
PR 11-AUG-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

Query Match 100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 5,1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 IVFPRYHKLMSVEYSQSMGHFQNRVNLVGDIFRNDGSI MLCQVRES DGNVTCS IHLGN 240
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Db	301	GNKSSVNSTVLVKNVTKTNPKEIKCHFCERCEGKHIVSPPIIVREVEEESKSEAT	360
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AC	AB017875;		
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DT	26-AUG-2003 (first entry)		
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DE	Novel human secreted and transmembrane protein PRO1387.		
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KW	Human; secreted and transmembrane protein; PRO; antiinflammatory;		
KW	antiarteriosclerotic; cardiact; anti-infertility; anti-HIV; cytostatic;		
KW	antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;		
KW	TNF-alpha release; cell proliferation; cell differentiation;		
KW	gene expression modulator; proteoglycan release; cytokine release;		
KW	tumour; inflammatory disease; organ failure; atherosclerosis;		
KW	cardiac injury; infertility; birth defect; premature aging; AIDS;		
KW	acquired immunodeficiency syndrome; cancer; diabetic complication;		
KW	chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;		
XX	bioreactor; tissue typing.		
OS	Homo sapiens.		
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PN	US2003032156-A1.		
XX			
PD	13-FEB-2003.		
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PF	06-MAY-2002; 2002US-00140474.		
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PR	31-MAR-1997; 97WO-US005230.		
PR	12-JUN-1998; 98WO-US012456.		
PR	14-JUN-1998; 98WO-US014552.		
PR	28-AUG-1998; 98WO-US017898.		
PR	10-SEP-1998; 98WO-US018824.		
PR	14-SEP-1998; 98WO-US019093.		
PR	14-SEP-1998; 98WO-US019177.		
PR	16-SEP-1998; 98WO-US019330.		
PR	17-SEP-1998; 98WO-US019437.		
PR	07-OCT-1998; 98WO-US021141.		
PR	29-OCT-1998; 98WO-US022991.		
PR	20-NOV-1998; 98WO-US022992.		
PR	01-DEC-1998; 98WO-US024855.		
PR	05-JAN-1999; 98WO-US000106.		
PR	08-MAR-1999; 98WO-US005028.		
PR	10-MAR-1999; 98WO-US005190.		
PR	20-APR-1999; 98WO-US008615.		
PR	14-MAY-1999; 98WO-US010733.		
PR	02-JUN-1999; 98WO-US012252.		
PR	01-SEP-1999; 98WO-US020111.		
PR	08-SEP-1999; 98WO-US020594.		
PR	13-SEP-1999; 98WO-US020944.		
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PR	05-OCT-1999; 98WO-US021547.		
PR	29-NOV-1999; 98WO-US023089.		
PR	30-NOV-1999; 98WO-US028313.		

PR	30-NOV-1999;	99WO-US028409.
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PR	02-DEC-1999;	99WO-US028634.
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PR	02-DEC-1999;	99WO-US028564.
PR	02-DEC-1999;	99WO-US028565.
PR	16-DEC-1999;	99WO-US030095.
PR	20-DEC-1999;	99WO-US030911.
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PR	22-DEC-1999;	99WO-US030720.
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PR	05-JAN-2000;	2000WO-US000219.
PR	06-JAN-2000;	2000WO-US000277.
PR	11-FEB-2000;	2000WO-US000376.
PR	18-FEB-2000;	2000WO-US003565.
PR	18-FEB-2000;	2000WO-US004341.
PR	22-FEB-2000;	2000WO-US004342.
PR	24-FEB-2000;	2000WO-US004414.
PR	24-FEB-2000;	2000WO-US004914.
PR	24-FEB-2000;	2000WO-US005004.
PR	01-MAR-2000;	2000WO-US005601.
PR	02-MAR-2000;	2000WO-US005746.
PR	10-MAR-2000;	2000WO-US005841.
PR	10-MAR-2000;	2000WO-US006319.
PR	15-MAR-2000;	2000WO-US006884.
PR	20-MAR-2000;	2000WO-US007377.
PR	21-MAR-2000;	2000WO-US007532.
PR	30-MAR-2000;	2000WO-US008439.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014941.
PR	30-MAY-2000;	2000WO-US015264.
PR	02-JUN-2000;	2000WO-US015264.
PR	28-JUL-2000;	2000WO-US020710.
PR	11-AUG-2000;	2000WO-US022031.
PR	23-AUG-2000;	2000WO-US023322.
PR	24-AUG-2000;	2000WO-US023328.
PR	08-NOV-2000;	2000WO-US030952.
PR	10-NOV-2000;	2000WO-US030873.
PR	01-DEC-2000;	2000WO-US032878.
PR	20-DEC-2000;	2000US-00747259.
PR	20-DEC-2000;	2000WO-US034956.
PR	28-FEB-2001;	2001US-00796498.
PR	28-FEB-2001;	2001WO-US006520.
PR	01-MAR-2001;	2001WO-US006566.
PR	09-MAR-2001;	2001US-00802706.
PR	14-MAR-2001;	2001US-00808689.
PR	22-MAR-2001;	2001US-00816744.
PR	05-APR-2001;	2001US-00828366.
PR	10-MAY-2001;	2001US-00854208.
PR	18-MAY-2001;	2001US-00854280.
PR	18-MAY-2001;	2001US-00860216.
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PR	25-MAY-2001;	2001WO-US017092.
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PR	01-JUN-2001;	2001WO-US017800.
PR	05-JUN-2001;	2001US-00874503.
PR	14-JUN-2001;	2001US-00882636.
PR	19-JUN-2001;	2001US-00886342.
PR	20-JUN-2001;	2001WO-US019692.
PR	21-JUN-2001;	2001US-00887879.
PR	22-JUN-2001;	2001WO-US020116.
PR	29-JUN-2001;	2001WO-US021066.
PR	09-JUL-2001;	2001WO-US021735.
PR	18-JUL-2001;	2001US-00908827.
PR	06-AUG-2001;	2001US-00924419.
PR	09-AUG-2001;	2001US-00927796.
PR	16-AUG-2001;	2001US-00931836.
PR	19-DEC-2001;	2001US-00028072.
XX	(GETH) GENENTECH INC.	
PA		
XX		

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
DR WPI; 2003-341980/32.
XX N-PSDB; ACD24112.
XX
XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 520; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
XX Sequence 394 AA;
Query Match 100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 5,1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AC ABU60611;
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DT 01-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein, #170.
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KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
KW diagnostic; therapeutic; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002160384-A1.
XX
PD 31-OCT-2002.
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PF 14-NOV-2001; 2001US-00992598.
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PR 16-JUN-1997; 97US-0049787P.
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PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
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PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.

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CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
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SQ Sequence 394 AA;

Query Match      100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.le-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61  PGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEAQGTVICIRL 120
Db      61  PGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEAQGTVICIRL 120

Qy      121  KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHTVKEWIFSGRRAKEE 180
Db      121  KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHTVKEWIFSGRRAKEE 180

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Db      181  IVFRYYHKLMSVEYSQSGWHFQNRVNLVGDIFRNDGSIIMLGVRSDGGNYTCSIHLGN 240

Qy      241  LVFKKTVLHVSPPEPTLVTPAALRPLVLGGNOLVIIVGIVCATILLPLVLIIVKTC 300
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05-JAN-1999;	99WO-US000106.	
08-MAR-1999;	99WO-US005028.	
02-JUN-1999;	99WO-US012252.	
15-SEP-1999;	99WO-US021090.	
30-NOV-1999;	99WO-US021547.	
01-DEC-1999;	99WO-US028313.	
01-DEC-1999;	99WO-US028634.	
16-DEC-1999;	99WO-US030095.	
20-DEC-1999;	99WO-US030911.	
05-JAN-2000;	2000WO-US000219.	
06-JAN-2000;	2000WO-US000376.	
11-FEB-2000;	2000WO-US003565.	
18-FEB-2000;	2000WO-US004341.	
22-FEB-2000;	2000WO-US004414.	
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24-FEB-2000;	2000WO-US005004.	
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15-MAY-2000;	2000WO-US013358.	
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22-MAY-2000;	2000WO-US014042.	
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02-JUN-2000;	2000WO-US015264.	
28-JUL-2000;	2000WO-US020710.	
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08-NOV-2000;	2000WO-US030952.	
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28-AUG-2001;	2001US-00941992.	
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XX	(GETH) GENENTECH INC.	
XX	Askenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;	
XX	Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;	
PPI	Grimaldi JC, Gurney AP, Khlavin LV, Napier MA, Pan J, Paoni NF;	
PPI	Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;	
PPI	Zhang Z;	
XX		
XX	WPI: 2003-288106/28.	
DR	N-PSDB; AEX90370.	
XX		
PPT	New transmembrane polypeptides and nucleic acids encoding the	
PPT	polypeptides, useful in gene therapy, in chromosome identification, as	
PPT	chromosome markers, or in generating probes.	
XX		
XX	Claim 12; Fig 304; 650pp; English.	
PS		
XX		
XX	The invention discloses isolated PRO secreted/transmembrane polypeptides	
CC	comprising a sequence without signal peptide and the nucleic acid	
CC	encoding them. The polypeptides can be used to raise antibodies that	
CC	specifically bind to the PRO polypeptide, for linking a bioactive	
CC	molecule to a cell expressing a PRO protein and for modulating at least	
CC	one biological activity of a cell. The PRO polypeptides or	
CC	polynucleotides are also useful in gene therapy, in chromosome	
CC	identification, as chromosome markers, or in generating probes. The PRO	
CC	polypeptides are useful as molecular markers for protein electrophoresis,	
CC	and the isolated nucleic acids may be used for recombinantly expressing	
CC	those markers. The PRO polypeptides and nucleic acids may also be used in	
CC	tissue typing. Anti-PRO antibodies are useful in diagnostic assays for	
CC	PRO, and in affinity purification of PRO from recombinant cell culture or	
CC	natural sources. The sequences presented in ABU60478-ABU60624 are the PRO	
CC	polynucleotides of the invention. Note: The sequence data for this patent	

29/11/20

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Perfect score: 1630
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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1630	100.0	1630	3 AAZ65110	AAZ65110 Membrane-
2	1630	100.0	1630	3 AAA77683	AAA77683 Human PRO
3	1630	100.0	1630	5 AAS21503	AAS21503 Human CDN
4	1630	100.0	1630	5 AAF44256	AAF44256 Human PRO
5	1630	100.0	1630	6 ABK33633	ABK33633 cDNA enco
6	1630	100.0	1630	6 ABL88188	ABL88188 Human PRO
7	1630	100.0	1630	6 ABL95677	ABL95677 Human ang
8	1630	100.0	1630	7 ABX77981	ABX77981 Human PRO
9	1630	100.0	1630	7 ABX80393	ABX80393 Novel hum
10	1630	100.0	1630	7 ACA69299	ACA69299 Human CDN
11	1630	100.0	1630	7 ACD24112	ACD24112 Novel hum
12	1630	100.0	1630	7 ABX90370	ABX90370 Human sec
13	1630	100.0	1630	7 ACA66938	ACA66938 cDNA enco
14	1630	100.0	1630	7 ACD86690	ACD86690 Novel hum
15	1630	100.0	1630	7 ABX64216	ABX64216 cDNA enco
16	1630	100.0	1630	7 ACA67253	ACA67253 cDNA enco
17	1630	100.0	1630	7 ACA64438	ACA64438 Novel hum
18	1630	100.0	1630	7 ACA03862	ACA03862 cDNA enco
19	1630	100.0	1630	7 ABX89400	ABX89400 DNA enco
20	1630	100.0	1630	7 ABX80897	ABX80897 Human sec
21	1630	100.0	1630	7 ACD44406	ACD44406 cDNA enco
22	1630	100.0	1630	7 ACD42054	ACD42054 Human sec
23	1630	100.0	1630	7 ACA68594	ACA68594 Novel hum

ALIGNMENTS

RESULT 1
AAZ65110
ID AAZ65110 standard; cDNA; 1630 BP.
XX
AC AAZ65110;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1387 encoding cDNA.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX
OS Homo sapiens.
XX
PN WO963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088741P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088811P.

Abx79577 Human sec
Aca93598 Novel hum
Abx81280 Novel hum
Aca04283 Human CDN
Aca93096 Novel hum
Abx17180 Human PRO
Aca68035 Novel hum
Aca88484 Human sec
Acdb1991 cDNA enco
Ada46038 Novel hum
Ada76469 Human PRO
Abt44323 Human PRO
Ada19119 Human PRO
Ada61742 Homo sapi
Adb19527 Novel hum
Adb28068 cDNA enco
Ada86547 Novel hum
Adb16111 Human PRO
Ada37932 Human CDN
Ada47897 Human PRO
Ada21618 Human CDN
Ada10405 Human CDN

1 CGGCTCGAGTCAGCTGGGGAGATTTTCAGTGCATTCCTCCCTCGGTCTTTCATC 60
61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACCTGAAACTCATCTCTGTCGCAAGT 120
61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTGGCCACCTGAAACTCATCTCTGTCGCAAGT 120
121 TTACTGGATTAATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACATC 180
121 TTACTGGATTAATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACATC 180
181 CATGTGGTGATTCAGTCTCTGATGGGATGTTTTCAGAGCAGAGAGCAAAATGTATA 240
181 CATGTGGTGATTCAGTCTCTGATGGGATGTTTTCAGAGCAGAGAGCAAAATGTATA 240
241 TTCAAGATAGACTGACTCTGTCACAGAGAGCAGCAAGGAGCTGACCTGATATAC 300
241 TTCAAGATAGACTGACTCTGTCACAGAGAGCAGCAAGGAGCTGATATGCTATAC 300
301 TATTACTCCAACTCTCAGTGTGCTTATGGGGCTTCCAGAACCCGCTACCTGATGGG 360
301 TATTACTCCAACTCTCAGTGTGCTTATGGGGCTTCCAGAACCCGCTACCTGATGGG 360
361 GACATCTTATGCAATGATGCTCTCTCTGCTCCAAAGATGTGCAAGAGCTGACCAAGG 420
361 GACATCTTATGCAATGATGCTCTCTCTGCTCCAAAGATGTGCAAGAGCTGACCAAGG 420
421 ACCTATATCTGTGAAATCCGCTCAAGGGAGAGCAGCTGTTCAAGAGCGGTGTA 480
421 ACCTATATCTGTGAAATCCGCTCAAGGGAGAGCAGCTGTTCAAGAGCGGTGTA 480
481 CTGCATGTGCTTCCAGAGAGCCCAAGAGCTCATGTGCTCATGTGGGTGGAATCATTCAG 540
481 CTGCATGTGCTTCCAGAGAGCCCAAGAGCTCATGTGCTCATGTGGGTGGAATCATTCAG 540
541 ATGGGATGTGTTTCCAGAGCAGAGAGTGAACACGTCGACCAAGGTAGATGATATTT 600
541 ATGGGATGTGTTTCCAGAGCAGAGAGTGAACACGTCGACCAAGGTAGATGATATTT 600
601 TCAGGAGCGCGCAAGAGGAGGATGTTATTTGTTACTACCAAACTCAGGATGTCT 660
601 TCAGGAGCGCGCAAGAGGAGGATGTTATTTGTTACTACCAAACTCAGGATGTCT 660
661 GTGAGTACTCCAGAGCTGGGGCACTTCCAGAACTGTGTGACCTGTGGGGGACATT 720
661 GTGAGTACTCCAGAGCTGGGGCACTTCCAGAACTGTGTGACCTGTGGGGGACATT 720
721 TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAGATGAGGAAACTAC 780
721 TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAGATGAGGAAACTAC 780
781 ACCTGAGTATCCAGTACCTGAGGAGCTGTTTCAAGAAACCATTTGCTGATGTCAGC 840
781 ACCTGAGTATCCAGTACCTGAGGAGCTGTTTCAAGAAACCATTTGCTGATGTCAGC 840
841 CCGGAGAGCTCGAACTGTTGGGAAATGTTCTGTGCCCAATCTCTGCTGCTCCCTGTTCTG 900
841 CCGGAGAGCTCGAACTGTTGGGAAATGTTCTGTGCCCAATCTCTGCTGCTCCCTGTTCTG 900
901 AATCAGTTGTGATCATTTGGGAAATGTTCTGTGCCCAATCTCTGCTGCTCCCTGTTCTG 960
901 AATCAGTTGTGATCATTTGGGAAATGTTCTGTGCCCAATCTCTGCTGCTCCCTGTTCTG 960
961 ATATTGATCTGAGAGACTGTGGGAAATGTTCTGTGCCCAATCTCTGCTGCTCCCTGTTCTG 1020
961 ATATTGATCTGAGAGACTGTGGGAAATGTTCTGTGCCCAATCTCTGCTGCTCCCTGTTCTG 1020
1021 AAGAAACAGGAGAGACTTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGT 1080
1021 AAGAAACAGGAGAGACTTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGT 1080
1081 GAAGGGAGAGAAACACATTTTACTCCCCAATTAATTTGACGGGAGGTGATCCGAGGAAGAA 1140

1081 GAAGGGAGAGAAACACATTTTACTCCCCAATTAATTTGACGGGAGGTGATCCGAGGAAGAA 1140
1141 CCAAGTGAATAATCAGAGGCCACCTACATGACCAATGACACCCAGTTTGGCCCTTCTCTGAGG 1200
1141 CCAAGTGAATAATCAGAGGCCACCTACATGACCAATGACACCCAGTTTGGCCCTTCTCTGAGG 1200
1201 TCAGATCGGAACAACTCACTTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA 1260
1201 TCAGATCGGAACAACTCACTTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA 1260
1261 GCCTTTTGGAGAAATGGAGAGTCCCTTCACTCTCAGCAGCGGTGGAGACTCTCTCTCTGT 1320
1261 GCCTTTTGGAGAAATGGAGAGTCCCTTCACTCTCAGCAGCGGTGGAGACTCTCTCTCTGT 1320
1321 TGTCTCTGGGCCACTCTTACCAAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTGT 1380
1321 TGTCTCTGGGCCACTCTTACCAAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTGT 1380
1381 CTCAATGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGAC 1440
1381 CTCAATGTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGAC 1440
1441 AGCTCTCGAGGAAACAGGCTGCTCAGCGGAGGAGCATGAGCTTGGCTCTGGAGTGGG 1500
1441 AGCTCTCGAGGAAACAGGCTGCTCAGCGGAGGAGCATGAGCTTGGCTCTGGAGTGGG 1500
1501 ACATGCGCTTGGGAAACAGGCTGAGCTGAGTGGCCCTCAAAACCCCTTGGATCAGACC 1560
1501 ACATGCGCTTGGGAAACAGGCTGAGCTGAGTGGCCCTCAAAACCCCTTGGATCAGACC 1560
1561 CTCCTGTGGGCAAGGTTCTTAGTGGATGAGTTACTTGGGAGAAATCAGAGATAAAACCAA 1620
1561 CTCCTGTGGGCAAGGTTCTTAGTGGATGAGTTACTTGGGAGAAATCAGAGATAAAACCAA 1620
1621 CCCAAATCAA 1630
1621 CCCAAATCAA 1630

RESULT 2
AAA77683
ID AAA77683 standard; cDNA; 1630 BP.
XX
AC AAA77683;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human PRO1387 cDNA sequence SEQ ID NO:219.
XX
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
KW cytosolic; gene therapy; vaccine; ss.
OS Homo sapiens.
XX
PN WO200032221-A2.
XX
PD 08-JUN-2000.
XX
PF 30-NOV-1999; 99WO-US028313.
XX
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 12-JAN-1999; 99US-0115554P.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-OCT-1999; 99US-0162506P.
 XX (GETH) GENENTECH INC.
 XX PA
 XX PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
 PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
 PI Smith V, Watanabe CK, Williams PM, Wood WI;
 XX
 DR WPI; 2000-412154/35.
 DR P-PSDB; AAB24433.
 XX
 PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
 PT and treating diagnosing a cardiovascular, endothelial or angiogenic
 PT disorders in mammals.
 XX
 PS Claim 61; Fig 91; 315pp; English.
 XX
 CC The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder in mammals by
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,
 CC and for identifying agonists and antagonists of these processes. The
 CC nucleic acids and the proteins they encode may be used in the prevention,
 CC treatment and diagnosis of diseases associated with inappropriate PRO
 CC expression such as cardiovascular, endothelial or angiogenic disorders in
 CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
 CC example, the nucleic acids (NCs) and vectors containing them and the PRO
 CC polypeptide may be used to treat disorders associated with decreased PRO
 CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
 CC nucleotide and protein sequences used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1630; DB 3; Length 1630;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGCTCGAGTGCAGTGTGGGAGATTTTCAGTGCAATGGCTCCCTGGGTCTCTTCATC 60
 DB 1 CGGCTCGAGTGCAGTGTGGGAGATTTTCAGTGCAATGGCTCCCTGGGTCTCTTCATC 60
 QY 61 TTGGATTGAAAGTTGAGAGCAGCATGTTTCCCACTGAAACTCATCTCTGCTGCCAGTG 120
 DB 61 TTGGATTGAAAGTTGAGAGCAGCATGTTTCCCACTGAAACTCATCTCTGCTGCCAGTG 120
 QY 121 TTACTGGATTATTCCTGGGCTGAAATGCACTTTGAATGTTTCCCGCTGAGCTAACAGTC 180
 DB 121 TTACTGGATTATTCCTGGGCTGAAATGCACTTTGAATGTTTCCCGCTGAGCTAACAGTC 180
 QY 181 CATGTGGGTGATTGAGTCTGATGGATGTTTCCAGAGCAGACAGACAAATGTATA 240
 DB 181 CATGTGGGTGATTGAGTCTGATGGATGTTTCCAGAGCAGACAGACAAATGTATA 240
 QY 241 TTCAAGATAGACTGGACTCTGTCCAGGAGAGCAGCCCAAGACGAATATGTGCTATAC 300
 DB 241 TTCAAGATAGACTGGACTCTGTCCAGGAGAGCAGCCCAAGACGAATATGTGCTATAC 300
 QY 301 TATTACTCCAAATCTCAGTGTGCTATTTGGCGCTTCCAGAACCGGCTACACTTGATGGGG 360
 DB 301 TATTACTCCAAATCTCAGTGTGCTATTTGGCGCTTCCAGAACCGGCTACACTTGATGGGG 360
 QY 361 GACATCTTATGAATGAGTGGCTCTCTCCCTCCAGATGTCCAGAGGCTGACACAGGGA 420
 DB 361 GACATCTTATGAATGAGTGGCTCTCTCCCTCCAGATGTGCAAGAGGCTGACACAGGGA 420
 QY 421 ACCTATATCTGTGAAATCCGCTCAAAGGGGAGAGCCAGGTGTTTCAAGAAAGCGGTGTA 480

DB 421 ACCTATATCTGTGAAATCCGCTCAAAGGGGAGAGCCAGGTGTTTCAAGAAAGCGGTGTA 480
 QY 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGACTCATGTGTCATGTGGGTGATTCATTCAG 540
 DB 481 CTGCATGTGCTTCCAGAGGAGCCCAAGAGACTCATGTGTCATGTGGGTGATTCATTCAG 540
 QY 541 ATGGGATGTGTTTCCAGAGCAGACAGAAAGTGAACACACGTGACCAAGGTGAAATGATATTT 600
 DB 541 ATGGGATGTGTTTCCAGAGCAGACAGAAAGTGAACACACGTGACCAAGGTGAAATGATATTT 600
 QY 601 TCAGAGCGGCGGCAAAAGGAGAGATTTATTTTCGTTACTACCAAACTCAGGATGTCT 660
 DB 601 TCAGAGCGGCGGCAAAAGGAGAGATTTATTTTCGTTACTACCAAACTCAGGATGTCT 660
 QY 661 GTGGAGTACTCCAGAGACTGGGGCCACTTCCAGATCGTGTGAACCTGTGGGGGACATT 720
 DB 661 GTGGAGTACTCCAGAGACTGGGGCCACTTCCAGATCGTGTGAACCTGTGGGGGACATT 720
 QY 721 TTCCGCAATGACGGTTCATCATCTTCAAGGAGTGAGGAGTGCAGATGGAGGAACTAC 780
 DB 721 TTCCGCAATGACGGTTCATCATCTTCAAGGAGTGAGGAGTGCAGATGGAGGAACTAC 780
 QY 781 ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAAACCATTTGTCTCATGTGTCAGC 840
 DB 781 ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAAACCATTTGTCTCATGTGTCAGC 840
 QY 841 CCGAAGAGCTCGAAACACTGGTCAACCCGAGCCCTGAGGCTCTGGTCTTGGGTGGT 900
 DB 841 CCGAAGAGCTCGAAACACTGGTCAACCCGAGCCCTGAGGCTCTGGTCTTGGGTGGT 900
 QY 901 AATCAGTTGGTGATCATTTGTGGGAATTTCTGTGTCACAACTCTGCTCTCTCTG 960
 DB 901 AATCAGTTGGTGATCATTTGTGGGAATTTCTGTGTCACAACTCTGCTCTCTCTG 960
 QY 961 ATATTGATCTGGAAGAGACTGTGGAAATTAAGAGTTTCAGTGAATTTACAGTCTTGGTG 1020
 DB 961 ATATTGATCTGGAAGAGACTGTGGAAATTAAGAGTTTCAGTGAATTTACAGTCTTGGTG 1020
 QY 1021 AAGAACAGAGAGACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGAGTGT 1080
 DB 1021 AAGAACAGAGAGACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGAGTGT 1080
 QY 1081 GAAGGGGAGAAACACATTTACTTCCCAATAATTTGTACGGGAGGTGATCGAGGAAAGAA 1140
 DB 1081 GAAGGGGAGAAACACATTTACTTCCCAATAATTTGTACGGGAGGTGATCGAGGAAAGAA 1140
 QY 1141 CCAAGTGAATAATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCTTCTCTGAGG 1200
 DB 1141 CCAAGTGAATAATCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCTTCTCTGAGG 1200
 QY 1201 TCAGATCGGAACACTCTTTGAAAGGAGTCAAGTGGGGGAAATGCCAAACACACAGCAA 1260
 DB 1201 TCAGATCGGAACACTCTTTGAAAGGAGTCAAGTGGGGGAAATGCCAAACACACAGCAA 1260
 QY 1261 GCCTTTTCAGAGAGATGGAGAGTCCCTTTCATCTCAGACGCGGTGAGAGTCTCTCTG 1320
 DB 1261 GCCTTTTCAGAGAGATGGAGAGTCCCTTTCATCTCAGACGCGGTGAGAGTCTCTCTG 1320
 QY 1321 TGTGTCCTGGGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGTGTCTCTCTG 1380
 DB 1321 TGTGTCCTGGGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGTGTCTCTCTG 1380
 QY 1381 CTCATTGTTTGTGTCATACACTGAAGATGGAGAAATTTGGAGCTCGCAGAGACTGGAC 1440
 DB 1381 CTCATTGTTTGTGTCATACACTGAAGATGGAGAAATTTGGAGCTCGCAGAGACTGGAC 1440
 QY 1441 AGCTCTGGAGGAAACAGGCTCTGAGGGGAGGGAGTGAAGTGGCTCTGGAGTGGG 1500
 DB 1441 AGCTCTGGAGGAAACAGGCTCTGAGGGGAGGGAGTGAAGTGGCTCTGGAGTGGG 1500
 QY 1501 ACATGCGCTCGGGAACAGGCTGAGTGGCTCAACCCCGCTGATCAGAC 1560

Db 1501 AACTGGCCCTGGGAACAGGCTGAGTGGTCTCAAAACCCCGCTGGATCAGACC 1560
QY 1561 CTCTGTGGCAGGTTCTTAGTGGATGAGTACTGGAGAGATCAGAGTAAACCAA 1620
Db 1561 CTCTGTGGCAGGTTCTTAGTGGATGAGTACTGGAGAGATCAGAGTAAACCAA 1620
QY 1621 CCCAATCAA 1630
Db 1621 CCCAATCAA 1630

RESULT 3

AAS21503
ID AAS21503 standard; cDNA; 1630 BP.

XX AC AAS21503;
XX DT 24-OCT-2001 (first entry)
XX DE Human cDNA sequence encoding for PRO1387 polypeptide.
XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy; ss.
XX OS Homo sapiens.
XX PN WO200140466-A2.
XX PD 07-JUN-2001.

PF 01-DEC-2000; 2000WO-US032678.
XX 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US028565.
PR 20-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 30-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 05-JAN-2000; 99WO-US031274.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.

XX (GETH) GENENTECH INC.
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
XX Gerritsen WE, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-408281/43.
DR P-PSDB; AAU12431.

XX Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.

XX Claim 3; Fig 519; 813pp; English.

XX AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX

SQ Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match	Best Local Similarity	Score 1630;	DB 4;	Length 1630;
Matches 1630;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	
QY 1	CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTCCCTCCCTGGGTCTTTCATC	60		
Db 1	CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTCCCTCCCTGGGTCTTTCATC	60		
QY 61	TTGGATTGAAAGTTGAGAGCAGCATGTTTGCCCACTGAAACTCATCTGTCGCAAGT	120		
Db 61	TTGGATTGAAAGTTGAGAGCAGCATGTTTGCCCACTGAAACTCATCTGTCGCAAGT	120		
QY 121	TTACTGGATTATTCCTTTGGGCTGAATGACTTGTAATGTTTCCCGCTGAGCTAACAGTC	180		
Db 121	TTACTGGATTATTCCTTTGGGCTGAATGACTTGTAATGTTTCCCGCTGAGCTAACAGTC	180		
QY 181	CATGTGGGTGATTTCAGCTCTGATGGGATGTTTTCAGAGCAGACAGAAATGTATA	240		
Db 181	CATGTGGGTGATTTCAGCTCTGATGGGATGTTTTCAGAGCAGACAGAAATGTATA	240		
QY 241	TTCAAGATACATGGACTCTGTACAGGAGAGCAGCCCAAGGACGAATATGTCTATAC	300		
Db 241	TTCAAGATACATGGACTCTGTACAGGAGAGCAGCCCAAGGACGAATATGTCTATAC	300		
QY 301	TATTACTCCAAATCTCAGTGTGCTTATTTGGGCGCTTCCAGAACCCGCTACACTTGATGGG	360		
Db 301	TATTACTCCAAATCTCAGTGTGCTTATTTGGGCGCTTCCAGAACCCGCTACACTTGATGGG	360		
QY 361	GACATCTTATGCAATGATGGCTCTCTCTCTCAAGATGTGCAAGAGGCTGACCCAGGA	420		
Db 361	GACATCTTATGCAATGATGGCTCTCTCTCTCAAGATGTGCAAGAGGCTGACCCAGGA	420		
QY 421	ACCTATATCTGTGAATCCGCTCAAGGGGAGCCAGGTGTTCAAGAGGCGGTGTA	480		

Db 421 ACCATATCTGTGAAATCCGCTCAAGGGAGAGCCAGGTGTTCAAGAAAGCGGTGTA 480
Qy 481 CTGCATGTGCTTCCAGAGAGAGCCAAAGAGCTCATGTCCTGAGTGGGTGAGTATTCAG 540
Db 481 CTGCATGTGCTTCCAGAGAGAGCCAAAGAGCTCATGTCCTGAGTGGGTGAGTATTCAG 540
Qy 541 ATGGGATGTGTTTCCAGAGACAGAAAGTGAACACAGTGAACCAAGTGAATGATATTT 600
Db 541 ATGGGATGTGTTTCCAGAGACAGAAAGTGAACACAGTGAACCAAGTGAATGATATTT 600
Qy 601 TCAGACCGCGCGCAAGAGAGAGATTTGATTTTCTGTTACTACCAAACTCAGAGTGTCT 660
Db 601 TCAGACCGCGCGCAAGAGAGAGATTTGATTTTCTGTTACTACCAAACTCAGAGTGTCT 660
Qy 661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAACTCGTGTGAACCTGGTGGGGACATT 720
Db 661 GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAACTCGTGTGAACCTGGTGGGGACATT 720
Qy 721 TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAAGTGGAGAACTAC 780
Db 721 TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAAGTGGAGAACTAC 780
Qy 781 ACTTCAGTATCCACTAGGAACTCGTGTTCAGAAACCAATTTGCTGCATGTTCAGC 840
Db 781 ACTTCAGTATCCACTAGGAACTCGTGTTCAGAAACCAATTTGCTGCATGTTCAGC 840
Qy 841 CCGGAGAGCCTCGAACTGTGAGCCCGGAGCCCTGAGGCTCTGTCTTGGGTGT 900
Db 841 CCGGAGAGCCTCGAACTGTGAGCCCGGAGCCCTGAGGCTCTGTCTTGGGTGT 900
Qy 901 AATCAGTTGGTCACTTGTGGAACTGTCTGTCACAACTCCTGCTGCTCCTGTTCTG 960
Db 901 AATCAGTTGGTCACTTGTGGAACTGTCTGTCACAACTCCTGCTGCTCCTGTTCTG 960
Qy 961 ATATTGATCGTGAAGAACTGTGGAATAAGAGTTTCAAGTGAATTTCAAGTCTTGGTG 1020
Db 961 ATATTGATCGTGAAGAACTGTGGAATAAGAGTTTCAAGTGAATTTCAAGTCTTGGTG 1020
Qy 1021 AAGAACCAAGAACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGT 1080
Db 1021 AAGAACCAAGAACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGT 1080
Qy 1081 GAAGGGAGAAACACATTTACTCCCAATTTGTACGGAGTGTACGAGGAAGAA 1140
Db 1081 GAAGGGAGAAACACATTTACTCCCAATTTGTACGGAGTGTACGAGGAAGAA 1140
Qy 1141 CCAAGTGAAATTCAGAGCCACTACATGACCATGCCACCTTTGGCCTTCTCTGAGG 1200
Db 1141 CCAAGTGAAATTCAGAGCCACTACATGACCATGCCACCTTTGGCCTTCTCTGAGG 1200
Qy 1201 TCAGATCGGAAACACTCTTGAATAAAGTCAAGTGGGGGAATGCCAAAACACAGCAA 1260
Db 1201 TCAGATCGGAAACACTCTTGAATAAAGTCAAGTGGGGGAATGCCAAAACACAGCAA 1260
Qy 1261 GCCTTTTGAGAAATGAGAGTCCCTTCACTCAGCAGGGTGGAGACTCTCTCTGTG 1320
Db 1261 GCCTTTTGAGAAATGAGAGTCCCTTCACTCAGCAGGGTGGAGACTCTCTCTGTG 1320
Qy 1321 TGTGCTCTGGGCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTGT 1380
Db 1321 TGTGCTCTGGGCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTGT 1380
Qy 1381 CTCAATGTTTGGTCAATACACTAGATGAGAAATTTGGAGCTTGGAGAGACTGGAC 1440
Db 1381 CTCAATGTTTGGTCAATACACTAGATGAGAAATTTGGAGCTTGGAGAGACTGGAC 1440
Qy 1441 AGCTCTGGAGAAACAGGCTCTGAGGGAGGGAGCATGCACTTGGCTCTGGAGTGGG 1500
Db 1441 AGCTCTGGAGAAACAGGCTCTGAGGGAGGGAGCATGCACTTGGCTCTGGAGTGGG 1500
Qy 1501 ACACCTGCGCTTGGGAAACAGGCTGAGTGTGAGTGGCTTCAACCCCGCTTGGATTCAGACC 1560

Db 1501 ACACCTGCGCTTGGGAAACAGGCTGAGTGTGAGTGGCTTCAACCCCGCTTGGATTCAGACC 1560
Qy 1561 CTCCTGTGGGAGAGGTTCTTAGTGTGATCAGTTACTTGGGAAGATCAGAGATAAAACCAA 1620
Db 1561 CTCCTGTGGGAGAGGTTCTTAGTGTGATCAGTTACTTGGGAAGATCAGAGATAAAACCAA 1620
Qy 1621 CCCAAATCAA 1630
Db 1621 CCCAAATCAA 1630
RESULT 4
AAF44256
ID AAF44256 standard; cDNA; 1630 BP.
XX
AC AAF44256;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1387 (UNQ722) nucleotide sequence SEQ ID NO:421.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay; ss.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149196P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US030095.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, KJavlin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR P-PSDB; AAB65287.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX

Claim 2; Fig 303; 935pp; English.

The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytosolic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF4470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to AAF65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 5; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CGGCTCGAGTCAGCTGGGAGATTTTCAGTGCATTTGCTCCCTGGGTCTTTCATC 60
DB 1 CGGCTCGAGTCAGCTGGGAGATTTTCAGTGCATTTGCTCCCTGGGTCTTTCATC 60
QY 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTTCGCCACTGAACTCATCTGTCGCAAGT 120
DB 61 TTGGATTTGAAAGTTGAGAGCAGCATGTTTTCGCCACTGAACTCATCTGTCGCAAGT 120
QY 121 TTACTGGATTTATCTTGGGCTGAATGACATTTGAATGTTTCCCGCTGAGTAAACAGTC 180
DB 121 TTACTGGATTTATCTTGGGCTGAATGACATTTGAATGTTTCCCGCTGAGTAAACAGTC 180
QY 181 CATGTGGGTGATTCAGCTCTGATGGGATGTTTTCAGAGCAGACAGAAATGATATA 240
DB 181 CATGTGGGTGATTCAGCTCTGATGGGATGTTTTCAGAGCAGACAGAAATGATATA 240
QY 241 TTCAGATAGACTGACCTGTCCAGGAGAGCAGCAGCAGGAGTACATTTGATGGG 300
DB 241 TTCAGATAGACTGACCTGTCCAGGAGAGCAGCAGCAGGAGTACATTTGATGGG 300
QY 301 TATTACTCAATCTCAGTGTGCTATTTGGGCGCTTCCAGAACCGGTACATTTGATGGG 360
DB 301 TATTACTCAATCTCAGTGTGCTATTTGGGCGCTTCCAGAACCGGTACATTTGATGGG 360
QY 361 GACATCTTATGCAATGATGGTCTCTCTGCTCCAAAGATGTGCAAGAGGCTGACAGGGA 420
DB 361 GACATCTTATGCAATGATGGTCTCTCTGCTCCAAAGATGTGCAAGAGGCTGACAGGGA 420
QY 421 ACCTATATCTGTGAAATCCGCTCAAAGGGAGAGCAGGAGTTCNAGAAGCGGTGTA 480
DB 421 ACCTATATCTGTGAAATCCGCTCAAAGGGAGAGCAGGAGTTCNAGAAGCGGTGTA 480
QY 481 CTGATGTGCTTCCAGAGAGCCCAAGAGCTCATGTGCTCCATGTGGGTGATTCATTCAG 540
DB 481 CTGATGTGCTTCCAGAGAGCCCAAGAGCTCATGTGCTCCATGTGGGTGATTCATTCAG 540
QY 541 ATGGGATGTGTTTCCAGAGCAGAGAGTGAAACACGTGACCAAGGTAGATGATATTT 600
DB 541 ATGGGATGTGTTTCCAGAGCAGAGAGTGAAACACGTGACCAAGGTAGATGATATTT 600
QY 601 TCAGAGCGCGCGCAAGAGGAGATTTGTTTCTGTTACTACCAAACTCAGATGCT 660
DB 601 TCAGAGCGCGCGCAAGAGGAGATTTGTTTCTGTTACTACCAAACTCAGATGCT 660
QY 661 GTGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATT 720
DB 661 GTGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATT 720
QY 721 TTCGGCAATGACGGTTCATCATGCTTCAAGAGTGGGGAGTCAGATGGAGAAATCTAC 780
DB 721 TTCGGCAATGACGGTTCATCATGCTTCAAGAGTGGGGAGTCAGATGGAGAAATCTAC 780
```

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DB 721 TTCCGCAATGACGGTTCATCATGCTTCAAGAGTGGGGAGTCAGATGGAGAAATCTAC 780
QY 781 ACTGTCAGTATCCACTAGGAAACCTGGTGTGTTCAAGAAACCACTTGTGTCATGTGTCAGC 840
DB 781 ACTGTCAGTATCCACTAGGAAACCTGGTGTGTTCAAGAAACCACTTGTGTCATGTGTCAGC 840
QY 841 CCGGAGAGCCTCGAACACTGTGTGACCCCGGAGCCCTGAGGCTCTGTGTTGGTGGT 900
DB 841 CCGGAGAGCCTCGAACACTGTGTGACCCCGGAGCCCTGAGGCTCTGTGTTGGTGGT 900
QY 901 AATCAGTGTGTCATGATGTCGGAATGTCGTGACCAATCTGTCGTCCTCCCTGTCG 960
DB 901 AATCAGTGTGTCATGATGTCGGAATGTCGTGACCAATCTGTCGTCCTCCCTGTCG 960
QY 961 ATATTGATGTCGTAAGAGACCTGTGGAATAAAGAGTTTCAGTGAATTTCTACAGTCTTGGTG 1020
DB 961 ATATTGATGTCGTAAGAGACCTGTGGAATAAAGAGTTTCAGTGAATTTCTACAGTCTTGGTG 1020
QY 1021 AAGAACACGAGAGCACTAATCCAGAGATAAAGAAACCTTGCATTTTGAAGATGT 1080
DB 1021 AAGAACACGAGAGCACTAATCCAGAGATAAAGAAACCTTGCATTTTGAAGATGT 1080
QY 1081 GAAAGGAGAAACACATTTTACTCCCAATAATTTGTACGGAGGTGATCGAGGAAGAA 1140
DB 1081 GAAAGGAGAAACACATTTTACTCCCAATAATTTGTACGGAGGTGATCGAGGAAGAA 1140
QY 1141 CCAAGTGAATAATCAGAGCCACCTTACATGACCATGACCCAGTTCCTCTGAGG 1200
DB 1141 CCAAGTGAATAATCAGAGCCACCTTACATGACCATGACCCAGTTCCTCTGAGG 1200
QY 1201 TCAGATCGGAAACACTCACTTGAATAAAGTCAGTGGGGAATGCCAAAAACACAGAA 1260
DB 1201 TCAGATCGGAAACACTCACTTGAATAAAGTCAGTGGGGAATGCCAAAAACACAGAA 1260
QY 1261 GCCTTTTGAAGAATGAGAGTCCCTTCACTCAGCAGCGGTGAGACTCTCTCTG 1320
DB 1261 GCCTTTTGAAGAATGAGAGTCCCTTCACTCAGCAGCGGTGAGACTCTCTCTG 1320
QY 1321 TGTGTCCTGGCCACTCTTACAGTGAATTTTCAAGTCTCCCGCTCTCCAGCTGTCTCTCTGT 1380
DB 1321 TGTGTCCTGGCCACTCTTACAGTGAATTTTCAAGTCTCCCGCTCTCCAGCTGTCTCTCTGT 1380
QY 1381 CTCATTTGTTGGTCAATACACTGAAGATGGAATTTGGAGCCCTGGCAGAGAGACTGAC 1440
DB 1381 CTCATTTGTTGGTCAATACACTGAAGATGGAATTTGGAGCCCTGGCAGAGAGACTGAC 1440
QY 1441 AGCTCTGGAGAAACAGGCTCTCAGGGGAGGAGCATGACCTTGGCTCTGGAGTGGG 1500
DB 1441 AGCTCTGGAGAAACAGGCTCTCAGGGGAGGAGCATGACCTTGGCTCTGGAGTGGG 1500
QY 1501 ACATGGCCCTGGAAACAGGCTCAGCTGAGTGGCTCAAACCCCGCTTGGATCAGACC 1560
DB 1501 ACATGGCCCTGGAAACAGGCTCAGCTGAGTGGCTCAAACCCCGCTTGGATCAGACC 1560
QY 1561 CTCCTGTCGAGGCTTCTTAGTGATGAGTACTGGAGAGATCAGAGATAAAACCA 1620
DB 1561 CTCCTGTCGAGGCTTCTTAGTGATGAGTACTGGAGAGATCAGAGATAAAACCA 1620
QY 1621 CCCAAATCAA 1630
DB 1621 CCCAAATCAA 1630
```

RESULT 5
ABK33633
ID ABK33633 standard; cDNA; 1630 BP.

XX ABK33633;

AC ABK33633;

XX 08-MAY-2002 (first entry)

XX cDNA encoding human PRO protein, Seq ID No 195.

KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.

XX Homo sapiens.

XX WO200208288-A2.

XX 31-JAN-2002.

XX 29-JUN-2001; 2001WO-US021066.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220585P.

XX 25-JUL-2000; 2000US-0220605P.

XX 25-JUL-2000; 2000US-0220607P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220638P.

XX 25-JUL-2000; 2000US-0220664P.

XX 25-JUL-2000; 2000US-0220666P.

XX 26-JUL-2000; 2000US-0220893P.

XX 28-JUL-2000; 2000WO-US020710.

XX 01-AUG-2000; 2000US-0222425P.

XX 22-AUG-2000; 2000US-0227133P.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 10-NOV-2000; 2000WO-US030873.

XX 28-NOV-2000; 2000US-0253646P.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2001; 2001WO-US006665.

XX 22-MAR-2001; 2001WO-US006744.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

XX 25-MAY-2001; 2001WO-US017092.

XX (GETH) GENENTECH INC.

XX Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

PI P-PSDB; AAU83689.

XX WPI; 2002-172001/22.

XX P-PSDB; AAU83689.

PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.

Claim 2; Fig 195; 359pp; English.

The invention relates to one hundred and twenty two nucleic acids
encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
encode human secreted proteins. The PRO nucleic acids, polypeptides,
agonists and antagonists are useful for treating a PRO related disorder.
The PRO polypeptides are useful for diagnosing tumors, especially lung
cancer, colon cancer, breast tumor, prostate tumor, rectal tumour or
liver tumour. The PRO polypeptides are useful for stimulating the
proliferation of, or gene expression, in pericyte cells, for stimulating
the proliferation or differentiation of chondrocyte cells, for
stimulating the release of tumour necrosis factor-alpha from human blood,
for stimulating or inhibiting the proliferation of normal human dermal
fibroblast cells. The PRO polypeptide may also be used as molecular
weight markers and for tissue typing. The PRO nucleic acids have
applications in molecular biology, including use as hybridisation probes,
and in chromosome and gene mapping. ABK3336-ABK33657 represent human PRO
protein coding sequences of the invention

Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1630;	DB 6;	Length 1630;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1630;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGATTCCTCCCTCCCTGGTCTCTTCATC	60	
DB	1	CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGATTCCTCCCTCCCTGGTCTCTTCATC	60	
QY	61	TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTCTGTCAGTG	120	
DB	61	TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTCTGTCAGTG	120	
QY	121	TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCCTGAGCTAACAGTC	180	
DB	121	TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCCTGAGCTAACAGTC	180	
QY	181	CATGTGGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCAGCAAGAAATGTATA	240	
DB	181	CATGTGGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCAGCAAGAAATGTATA	240	
QY	241	TTCAAGATAGACTGGACTCTGTCCAGAGAGCAGCCAGGACGAATATGTGTATAC	300	
DB	241	TTCAAGATAGACTGGACTCTGTCCAGAGAGCAGCCAGGACGAATATGTGTATAC	300	
QY	301	TATTAATCTCAATCTCAGTGTGCTTATGGGCGCTTCCAGAACCCGGTACATTTGATGGG	360	
DB	301	TATTAATCTCAATCTCAGTGTGCTTATGGGCGCTTCCAGAACCCGGTACATTTGATGGG	360	
QY	361	GACATCTTATGCAATGATGGCTCTCTCTGCTTCAAGATGTGCAAGAGCTACCCAGGA	420	
DB	361	GACATCTTATGCAATGATGGCTCTCTCTGCTTCAAGATGTGCAAGAGCTACCCAGGA	420	
QY	421	ACCTATATCTGTGAAATCCGCTCAAAAGGGAGAGCCAGGTCTTCAAGAGCGGTGTA	480	
DB	421	ACCTATATCTGTGAAATCCGCTCAAAAGGGAGAGCCAGGTCTTCAAGAGCGGTGTA	480	
QY	481	CTGCATGTGCTTCCAGAGAGCCCAAGAGCTCATGGTCCATGTGGGTGGATTCAG	540	
DB	481	CTGCATGTGCTTCCAGAGAGCCCAAGAGCTCATGGTCCATGTGGGTGGATTCAG	540	
QY	541	ATGGGATGTGTTTCCAGAGCAGAAAGTGAACAGCTGACCAAGTGAATGGATATTT	600	
DB	541	ATGGGATGTGTTTCCAGAGCAGAAAGTGAACAGCTGACCAAGTGAATGGATATTT	600	
QY	601	TCAGGACGGCGCGAAGAGGAGATTGTATTTGTTTACTTACCAACAATCTCAGGATGTCT	660	
DB	601	TCAGGACGGCGCGAAGAGGAGATTGTATTTGTTTACTTACCAACAATCTCAGGATGTCT	660	
QY	661	GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATT	720	
DB	661	GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGACATT	720	
QY	721	TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTGCAGATGAGGAACTAC	780	
DB	721	TTCCGCAATGACGGTTCATCATGCTTCAAGGAGTGAGGAGTGCAGATGAGGAACTAC	780	
QY	781	ACCTGAGTATCCACTAGGAACTGGTGTTCAGAAAAACCAATTTGCTGTCATGTGAGC	840	
DB	781	ACCTGAGTATCCACTAGGAACTGGTGTTCAGAAAAACCAATTTGCTGTCATGTGAGC	840	
QY	841	CCGAAAGAGCTCGAACACTGTGTGACCCCGGAGCCCTGAGGCTCTGGTCTTGGGTGGT	900	
DB	841	CCGAAAGAGCTCGAACACTGTGTGACCCCGGAGCCCTGAGGCTCTGGTCTTGGGTGGT	900	
QY	901	AATCAGTGTGATCATTTGTTGGAAATTTGTTGTCACCAATCTCTGCTGCTCCCTGTTCTG	960	
DB	901	AATCAGTGTGATCATTTGTTGGAAATTTGTTGTCACCAATCTCTGCTGCTCCCTGTTCTG	960	
QY	961	ATATTGATCGTGAAGAGACCTGTGGAATAAAGAGTTTCAGTGAATTCACAGTCTTGGTG	1020	
DB	961	ATATTGATCGTGAAGAGACCTGTGGAATAAAGAGTTTCAGTGAATTCACAGTCTTGGTG	1020	
QY	1021	AAGAACGAGAGAGACTAATCCAGAGATAAAGAAAAACCCCTGCCATTTTGAAGATGT	1080	

Db 1021 AAGAACACGAGAGAGTAATCCAGAGATAAAGAAACCCCTGCGCATTTTGAAGATGT 1080
 QY 1081 GAAGGGGAGAGAACACATTTTACTCCCAATAATTTGTACGGGAGGTGATCAGGAGAGAGAA 1140
 Db 1081 GAAGGGGAGAGAACACATTTTACTCCCAATAATTTGTACGGGAGGTGATCAGGAGAGAGAA 1140
 QY 1141 CCAAGTGAATAATCAGAGGCCACCTATCATGACCATGACCCAGTGTGGCTTCTCTGAGG 1200
 Db 1141 CCAAGTGAATAATCAGAGGCCACCTATCATGACCATGACCCAGTGTGGCTTCTCTGAGG 1200
 QY 1201 TCAGATCGGAACAACTCATCTGGAATAAGTCAAGTGGGGAGTCCAAAAACACAGCAAA 1260
 Db 1201 TCAGATCGGAACAACTCATCTGGAATAAGTCAAGTGGGGAGTCCAAAAACACAGCAAA 1260
 QY 1261 GCCTTTTGAGAGAAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTG 1320
 Db 1261 GCCTTTTGAGAGAAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTG 1320
 QY 1321 TGTGCTCTGGGCCACTTACCAAGTGAATTCAGACTCCCGCTCTCCAGCTGTCCTCTGT 1380
 Db 1321 TGTGCTCTGGGCCACTTACCAAGTGAATTCAGACTCCCGCTCTCCAGCTGTCCTCTGT 1380
 QY 1381 CTCATTGTTTGTCTAATACATGTAAGATGGAGAAATTTGGAGCTCGCAGAGAGACTGGAC 1440
 Db 1381 CTCATTGTTTGTCTAATACATGTAAGATGGAGAAATTTGGAGCTCGCAGAGAGACTGGAC 1440
 QY 1441 AGCTCTGGAGGAACAGGCTCTGAGGGGAGGAGGAGCATGGACTTTGGCTCTGGAGTGGG 1500
 Db 1441 AGCTCTGGAGGAACAGGCTCTGAGGGGAGGAGGAGCATGGACTTTGGCTCTGGAGTGGG 1500
 QY 1501 ACAGTGGCCCTGGGAACAGGCTGAGCTGAGTGGCTCAAAACCCCGCTTGGATCAGACC 1560
 Db 1501 ACAGTGGCCCTGGGAACAGGCTGAGCTGAGTGGCTCAAAACCCCGCTTGGATCAGACC 1560
 QY 1561 CTCCTGTGGGAGGTTCTTAGTGATGAGTACTGGGAAGATCAGAGATAAAACCAA 1620
 Db 1561 CTCCTGTGGGAGGTTCTTAGTGATGAGTACTGGGAAGATCAGAGATAAAACCAA 1620
 QY 1621 CCCAAATCAA 1630
 Db 1621 CCCAAATCAA 1630

RESULT 6

ABL88188
 ID ABL88188 standard; cDNA; 1630 BP.

XX AC ABL88188;

XX DT 16-MAY-2002 (first entry)

XX DE Human PRO1387 cDNA sequence SEQ ID NO:233.

XX KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping; gene; ss.

XX OS Homo sapiens.

XX PN WO200200690-A2.

XX PD 03-JAN-2002.

XX PF 20-JUN-2001; 2001WO-US019692.

XX PR 23-JUN-2000; 2000US-0213637P.

PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023322.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 10-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US030873.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 01-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001WO-US006520.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.

(GETH) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerecht ME, Goddard A;
 Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-090516/12.

P-PSDB; ABB84933.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 infarction), endothelial or angiogenic disorders in a mammal.

Claim 2; Fig 233; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 activities, and can be used in gene therapy. The PRO polynucleotides,
 proteins, agonists and antagonists are useful for treating or diagnosing
 a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 healing. The PRO polynucleotides have applications in molecular biology,
 including use as hybridisation probes, and in chromosome and gene
 mapping. ABL88259 to ABL88267 represent primers and probes used in the
 exemplification of the present invention

Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 6; Length 1630;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCTCCCTGGGTGCTTCATC 60

Db 1 CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCTCCCTGGGTGCTTCATC 60

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QY 121 TTACTGGAATTATCTTGGGCTGAATGACTTGAATGTTTCCAGAGCACAAGAAATGTATA 240
Db 121 TTACTGGAATTATCTTGGGCTGAATGACTTGAATGTTTCCAGAGCACAAGAAATGTATA 240
QY 181 CATGTGGGTGATTCAGCTCTGATGGATGTGTTTCCAGAGCACAAGAAATGTATA 240
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QY 241 TTCAAGATAGACTGGACTCTGTACCAAGAGAGCAGCGCAAGAGCGAATATGTGTATAC 300
Db 241 TTCAAGATAGACTGGACTCTGTACCAAGAGAGCAGCGCAAGAGCGAATATGTGTATAC 300
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QY 361 GACATCTTATGCAATGATGGCTCTCTCTGCTTCCAAGATGTGCAAGAGGCTGACCAAGGA 420
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QY 421 ACCTATATCTGTGAATCCGCTCAAGAGGAGAGCGAGTGTTCAGAGGCGGTGTA 480
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Db 481 CTGCAATGTCTTCCAGAGAGCGCCCAAGAGCTCATGCTTCCAGTGTGGTGGATTGATTGAG 540
QY 541 ATGGATGTGTTTCCAGAGCACAAGAGTGAACACGTCGACCAAGTAGAATGGATATT 600
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Db 601 TCAGAGCGCGCGCAAGAGAGAGATTGATTTCGTTACTACCAAACTCAGGATGCT 660
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QY 721 TTCCGCAATGACGGTTTCCATCATGCTTCAAGGAGTGAGGAGTCCAGATGGAGAACTAC 780
Db 721 TTCCGCAATGACGGTTTCCATCATGCTTCAAGGAGTGAGGAGTCCAGATGGAGAACTAC 780
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Db 1261 GCCTTTTGGAGAGAAATGGAGAGTCCCTTCACTCTCAGCAGCGGTGAGACTCTCTCTCTGT 1320
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QY 1621 CCCAAATCAA 1630
Db 1621 CCCAAATCAA 1630

RESULT 7
ABL95677
ID ABL95677 standard; cdna; 1630 BP.
XX ABL95677;
XX
XX
XX
XX 19-JUL-2002 (first entry)
DE Human angiogenesis related cdna PRO1387 SEQ ID NO: 233.
XX
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytoetic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic; gene; ss.
XX Homo sapiens.
XX
XX WO200208284-A2.
XX
XX 31-JAN-2002.
XX
XX 09-JUL-2001; 2001WO-US021735.
XX
XX 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222895P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANT/) PAN J.
PA (PAON/) PAONI N P.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski P, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye M;
DR P-PSDB; ABB95539.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 1; Fig 233; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention
XX
SQ Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 6; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CCGTCCAGTCCAGCTGTGGGAGATTTCAGTGCATTGCCCTCCCTGGTCTTTCATC 60
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Db 121 TTACTGGATTATTCCTTGGGCTGAAATGACTTGAATGTTTCCCGCTCAGCTAACAGTC 180
Qy 181 CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAACAAATGTATA 240
Db 181 CATGTGGGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAACAAATGTATA 240
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Db 241 TTCAGATAGACTGGACTCTGTCCAGAGAGAGCAGCCCAAGCAAAATGTGCTATAC 300
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Db 781 ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAAACCAATGCTGCTCATGTCAGC 840
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Db 841 CCGGAAGAGCCTCGAACACTGCTGACCCCGCAGCCCTGAGGCCCTCTGCTTGGTGGT 900
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				PR	04-JUN-1998;	98US-0088029P.
Db	1201	TCAGATCGAAACAACCTACTTTGAAAAAAGTCAGGTGGGGAATGCCAAAAACACAGCAA	1260	PR	04-JUN-1998;	98US-0088030P.
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				PR	10-JUN-1998;	98US-0088810P.
Db	1381	CTCATGTTTGTGTAATACATCTGAAGATGGAGAAATTTGAGCTGGCAGAGACTGGAC	1440	PR	10-JUN-1998;	98US-0088824P.
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Db	1501	ACACTGGCCCTGGGAACCAAGGCTGAGCTGAGTGGCTCAAAACCCCGCTGGATCAGACC	1560	PR	16-JUN-1998;	98US-0089514P.
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PR PR				PR	10-JUL-1998;	98US-0092472P.

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PR 26-AUG-1998; 98US-0097986P.
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PR 31-AUG-1998; 98US-0098525P.
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PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98US-0113296P.
PR 08-MAR-1999; 98US-0123957P.
PR 12-MAR-1999; 98US-0123957P.
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PR 15-SEP-1999; 98US-0150210P.
PR 15-SEP-1999; 98US-0150215P.
PR 08-OCT-1999; 98US-0158663P.
PR 30-NOV-1999; 98US-028313P.
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PR 20-DEC-1999; 98US-030911P.
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PR 06-JAN-2000; 2000US-0000376P.
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PR 02-MAR-2000; 2000US-0005841P.
PR 10-MAR-2000; 2000US-0006319P.
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QY 121 TTACTGGATTATTCCTTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC 180
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QY 181 CATGTGGGTGATTTCAGCTCTGATGGATGTTTCCAGAGCAGACAGAAATGTATA 240
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Db 1621 CCCAAATCAA 1630

RESULT 9
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ID ABX80393 standard; DNA; 1630 BP.

AC ABX80393;

XX 28-APR-2003 (first entry)

DE Novel human secreted or transmembrane protein PRO1384 DNA.

XX

Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
cardiac insufficiency disorder; cancer; tumour; immune response;
adrenal cortical capillary endothelial growth; c-fos induction;
vascular endothelial growth factor inhibition; VEGF inhibition;
endothelial cell growth inhibitor; T-lymphocytes stimulation;
retinal neurons cell survival; rod photoreceptor cell survival;
renal disorder; retinitis pigmentosa; kidney disorder;
mammalian kidney mesangial cell proliferation; Berger disease;
dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
chondrocyte redifferentiation; sports injury; arthritis; gene; ds.

Homo sapiens.

US2002132252-A1.

19-SEP-2002.

14-NOV-2001; 2001US-00990442.

16-JUN-1997; 97US-0049787P.
17-OCT-1997; 97US-0062250P.
05-NOV-1997; 97WO-US020069.
12-NOV-1997; 97US-0065186P.
24-NOV-1997; 97US-0066770P.
25-FEB-1998; 98US-0075945P.
20-MAR-1998; 98US-0078910P.
28-APR-1998; 98US-0083322P.
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16-SEP-1998; 98WO-US019330.
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07-OCT-1998; 98WO-US021141.
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1081 GAAGGGGAGAAACACATTTTACTCCCAATTAATTTGTACGGGAGGTGATCGAGGAAGAA 1140
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XX ACA69299;
XX ACA69299;
DT 26-JUN-2003 (first entry)
XX Human cDNA encoding secreted/transmembrane protein PRO1387.

DE Human; ss; gene; PRO; secreted protein; transmembrane protein;
XX Human; cardiac insufficiency disorders; angiogenesis; wound healing;
KW
KW

KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosum; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;
KW Crohn's disease; sports injury; arthritis.
XX Homo sapiens.
XX US2003032023-A1.
XX 13-FEB-2003.
XX 14-NOV-2001; 2001US-00990711.
XX 16-JUN-1997; 97US-0049787P.
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PR 06-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US000376.
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PR 22-FEB-2000; 2000WO-US004341.
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PR 02-MAR-2000; 2000WO-US005004.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US007377.
PR 17-MAY-2000; 2000WO-US013358.
PR 22-MAY-2000; 2000WO-US013705.
PR 30-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US014941.
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PR 11-AUG-2000; 2000WO-US022031.

Query Match 100.0%; Score 1630; DB 7; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
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Db 121 TTACTGGATTATTCCTTGGGCCTGAATGACTTTGAATGTTTCCCGCCCTGAGCTAACAGTC 180

Qy 181 CATGTGGGTGATTTCAGCTCTCATGGGATGTGTTTCCAGAGCAGAGCAAGAAATGTATA 240
Db 181 CATGTGGGTGATTTCAGCTCTCATGGGATGTGTTTCCAGAGCAGAGCAAGAAATGTATA 240

Qy 241 TTCAAGATAGACTGACTCTGTCCAGGAGCAGCCAGGACGATATGTGCTATAC 300
Db 241 TTCAAGATAGACTGACTCTGTCCAGGAGCAGCCAGGACGATATGTGCTATAC 300

Qy 301 TATTACTCCAATCTCAGTGTGCTTATGGGGCTTTCCAGAACCGGTACACTTGTATGGGG 360
Db 301 TATTACTCCAATCTCAGTGTGCTTATGGGGCTTTCCAGAACCGGTACACTTGTATGGGG 360
```

QY	361	GACATCTTATGCAATGATGGCTCTCTCTCTGCTCCAAAGATGTGCAAGAGGCTGACACAGGGA	420
Db	361	GACATCTTATGCAATGATGGCTCTCTCTCTGCTCCAAAGATGTGCAAGAGGCTGACACAGGGA	420
QY	421	ACCTATATCTGTGAAATCCGGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTA	480
Db	421	ACCTATATCTGTGAAATCCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTA	480
QY	481	CTGCATGTGCTTCCAGAGGAGCCAAAGAGCTCATGTGCTCCATGTGGTGGATGATTGATTCAG	540
Db	481	CTGCATGTGCTTCCAGAGAGGCCAAAGAGCTCATGTGCCATGTGGTGGATGATTGATTCAG	540
QY	541	ATGGGATGTGTTTTCCAGAGCACAGAAGTGAACACAGTGCACCAAGGTAGAAATCGATATTT	600
Db	541	ATGGGATGTGTTTTCCAGAGCACAGAAGTGAACACAGTGCACCAAGGTAGAAATCGATATTT	600
QY	601	TCAGGACGGCGCGCAAGAGGAGGATTTGTTTCGTCTACTACACAAACTCAGGATGTCT	660
Db	601	TCAGGACGGCGCGCAAGAGGAGGATTTGTTTCGTCTACTACACAAACTCAGGATGTCT	660
QY	661	GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGTGGGGGACATT	720
Db	661	GTGGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGTGGGGGACATT	720
QY	721	TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGAGTGCAGATGAGGAAACTAC	780
Db	721	TTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTGAGGAGTGCAGATGAGGAAACTAC	780
QY	781	ACCTGCAGTATCCACTTAGGGAACTGTGGTGTTCGAAGAAAACCAATGTGTGCAATGTCAGC	840
Db	781	ACCTGCAGTATCCACTTAGGGAACTGTGGTGTTCGAAGAAAACCAATGTGTGCAATGTCAGC	840
QY	841	CCGGAAGAGCTCGAACACTGGTCAGCCCGGACCCCTGAGGCTCTGCTTTGGGTGGT	900
Db	841	CCGGAAGAGCTCGAACACTGGTCAGCCCGGACCCCTGAGGCTCTGCTTTGGGTGGT	900
QY	901	AATCAGTTGGTGATCAATTTGGGAAATGTCTGTGCCCAATCTCTGCTGCTCCCTGTTCTG	960
Db	901	AATCAGTTGGTGATCAATTTGGGAAATGTCTGTGCCCAATCTCTGCTGCTCCCTGTTCTG	960
QY	961	ATAATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTTCAGTGAATTTCTACAGTCTTGGTG	1020
Db	961	ATAATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTTCAGTGAATTTCTACAGTCTTGGTG	1020
QY	1021	AAGBACACGAGAGAGACTAATCCAGAGATAAAGAAAACCCCTGCCAATTTTGAAGATGT	1080
Db	1021	AAGBACACGAGAGAGACTAATCCAGAGATAAAGAAAACCCCTGCCAATTTTGAAGATGT	1080
QY	1081	GAAGGGGAGAAACACATTTACTCCCCAATAATGTACGGGAGGTGATCGAGGAGAGAGAA	1140
Db	1081	GAAGGGGAGAAACACATTTACTCCCCAATAATGTACGGGAGGTGATCGAGGAGAGAGAA	1140
QY	1141	CAAAGTGAATAATCAGAGGCACTTACATGACCAATGCAACCAAGTTTGGCTTCTCTGAGG	1200
Db	1141	CAAAGTGAATAATCAGAGGCACTTACATGACCAATGCAACCAAGTTTGGCTTCTCTGAGG	1200
QY	1201	TCAGATCGGACCACTCACTTGAATAAAGTTCAGGTGGGGAAATGCCAABAAACACAGCAA	1260
Db	1201	TCAGATCGGACCACTCACTTGAATAAAGTTCAGGTGGGGAAATGCCAABAAACACAGCAA	1260
QY	1261	GCTTTTTCAGAGAAGATGAGAGTCCCTTCACTCAGCAGCGGTGGAGACTCTCTCCGTGTG	1320
Db	1261	GCTTTTTCAGAGAAGATGAGAGTCCCTTCACTCAGCAGCGGTGGAGACTCTCTCCGTGTG	1320
QY	1321	TGTGTCTGGGCCACTCTACCAAGTATTCAGACTCCCGTCTCTCCAGCTGTCTCTCTGT	1380
Db	1321	TGTGTCTGGGCCACTCTACCAAGTATTCAGACTCCCGTCTCTCCAGCTGTCTCTCTGT	1380
QY	1381	CTCATTTGTTGGTCAATACACTGAAGATGAGAAATTTGGAGCCCTGCGAGAGAGACTGGAC	1440
Db	1381	CTCATTTGTTGGTCAATACACTGAAGATGAGAAATTTGGAGCCCTGCGAGAGAGACTGGAC	1440
QY	1441	AGCTCTGGAGGAAACAGGCTCTGTGAGGGGAGGGGAGATGACATTTGGCTCTGAGTGGG	1500

RESULT 11

ACD24112

ID ACD24112 standard: cDNA: 1630 BP.

ACD24112:

XX
DT 26-AUG-2003 (first entry)XX
DE Novel human secreted and transmembrane protein PRO1387 cDNA.

XX	Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW	antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW	antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW	TNF-alpha release; cell proliferation; cell differentiation;
KW	gene expression modulator; proteoglycan release; cytokine release;
KW	tumour; inflammatory disease; organ failure; atherosclerosis;
KW	cardiac injury; infertility; birth defect; premature aging; AIDS;
KW	acquired immunodeficiency syndrome; cancer; diabetic complication;
KW	chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor
KW	bioreactor; tissue typing; gene: ss.

XX Homo sapiens.

XX
PN
US2003032156-A1

13-FEB-2003

06-MAY-2002: 2002US-00140474.

AA 31-MAR-1997: 97WO-US005230.

PR 14-JUL-1998: 98WO-US014552:

E2
E3
E4
E5

98WO-US018824;
98WO-US018824;
98WO-US018824;
98WO-US018824;

10-SEP-1998;
10-SEP-1998;
10-SEP-1998;
10-SEP-1998;

14-SEP-1998: 98WO-US019094: PR

PR 16-SEP-1998: 98WO-US019330.

PR 07-OCT-1998; 98WO-US021141.

PR 29-OCT-1998; 98WO-US022992.

PR 01-DEC-1998; 98WO-US025108.

PR 08-MAR-1999; 99WO-US005028.

PR 20-APR-1999; 99WO-US008615.

PR 02-JUN-1999; 99WO-US012252

PR 08-SEP-1999; 99WO-US020594.

PR 15-SEP-1999; 99WO-US021090.

PR 05-OCT-1999; 99WO-US023089.

PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001WO-US006520.
PR 28-FEB-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866026.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA

(GETH) GENENTECH INC.

XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-341980/32.
DR P-PSDB; ABO17875.
XX
DR New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 2; Fig 519; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide
XX

SQ Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

Query Match 100.0%; Score 1630; DB 7; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCTCCCTGGGTGCTTTCATC 60
DB 1 CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCTCCCTGGGTGCTTTCATC 60
QY 61 TTGGATTTCGAAGTTGAGAGCAGCATGTTTGGCCACTGAACTCATCTCTGCGCAGTG 120
DB 61 TTGGATTTCGAAGTTGAGAGCAGCATGTTTGGCCACTGAACTCATCTCTGCGCAGTG 120
QY 121 TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTC 180
DB 121 TTACTGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTC 180
QY 181 CATGFGGTGATTCAGTCTCTGATGGATGTGTTTCCAGAGCAGACAAATGTATA 240
DB 181 CATGFGGTGATTCAGTCTCTGATGGATGTGTTTCCAGAGCAGACAAATGTATA 240
QY 241 TTCAGATAGACTGGACTCTGTCCAGGAGACGCGCAAGGACGAATATGTCTATAC 300
DB 241 TTCAGATAGACTGGACTCTGTCCAGGAGACGCGCAAGGACGAATATGTCTATAC 300
QY 301 TATTACTCCAATCTCAGTGTGCTTATGGGCGCTTCCAGAACCGGTACCTTGTATGGGG 360
DB 301 TATTACTCCAATCTCAGTGTGCTTATGGGCGCTTCCAGAACCGGTACCTTGTATGGGG 360
QY 361 GACATCTTATCAATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA 420
DB 361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGA 420
QY 421 ACCTATATCTGTAATCCGGCTCAAGGGGAGAGCCAGGTGTTTCAAGAGCGGTGGTA 480

Db	421	ACCTATATCTGTGAAATCCGCTCAAGGGGAGAGCCAGTGTTCAAGAGCGGTGGTA	480	Db	1501	ACACTGGCCCTGGGAACCAAGGCTGAGCTGAGTGGCTCAAAACCCCGCTTGATCAGACC	1560
Qy	481	CTGCATGTCTTCCAGAGAGAGCCCAAGAGCTCATGGTCCATGTGGGTGGAATGATTCAG	540	Qy	1561	CTCCCTGTGGGACGGTCTTCTAGTGGATGAGTTACTGGGAAGAAATCAGAGATAAAACCAA	1620
Db	481	CTGCATGTCTTCCAGAGAGAGCCCAAGAGCTCATGGTCCATGTGGGTGGAATGATTCAG	540	Db	1561	CTCCCTGTGGGACGGTCTTCTAGTGGATGAGTTACTGGGAAGAAATCAGAGATAAAACCAA	1620
Qy	541	ATGGGATGTGTTTCCAGAGCAGCAGAGAGTGAACACAGTGCACCAAGTAGAATGGATATT	600	Qy	1621	CCCAAAATCAA	1630
Db	541	ATGGGATGTGTTTCCAGAGCAGCAGAGAGTGAACACAGTGCACCAAGTAGAATGGATATT	600	Db	1621	CCCAAAATCAA	1630
Qy	601	TCAGAGCGCGCGCAAGAGAGAGATTGTATTTCGTTCATACCAAACTCAGGATGTCT	660	RESULT 12			
Db	601	TCAGAGCGCGCGCAAGAGAGAGATTGTATTTCGTTCATACCAAACTCAGGATGTCT	660	ABX90370			
Qy	661	GTGGAGTACTCCAGAGCTGGGCCCACTTCCAGAAATCGTGTGAACTCGTGGGGGACATT	720	ID	ABX90370	standard; cDNA; 1630 BP.	
Db	661	GTGGAGTACTCCAGAGCTGGGCCCACTTCCAGAAATCGTGTGAACTCGTGGGGGACATT	720	XX	ABX90370;		
Qy	721	TTCCGCAATGACGGTTCCTATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGAACTAC	780	XX	01-MAY-2003	(first entry)	
Db	721	TTCCGCAATGACGGTTCCTATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGAACTAC	780	XX	Human secreted/transmembrane protein cDNA, #170.		
Qy	781	ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAGAAACCAATTCGTGTCATGTCAGC	840	XX	Human; gene; ss; PRO; secreted; transmembrane; signal peptide;		
Db	781	ACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAGAGAAACCAATTCGTGTCATGTCAGC	840	KW	pharmaceutical; diagnostic; therapeutic; gene therapy.		
Qy	841	CCGGAAGAGCCTCGAACACTGGTGACCCCGCAGCCCTGAGGCCCTCTGGTCTTTGGGTGGT	900	XX	Homo sapiens.		
Db	841	CCGGAAGAGCCTCGAACACTGGTGACCCCGCAGCCCTGAGGCCCTCTGGTCTTTGGGTGGT	900	XX	US2002160384-A1.		
Qy	901	AATCAGTGGTGATCATTTGGGAATTTGTCGTCACCAATCTGTCCTCCCTGTTCTG	960	XX	31-OCT-2002.		
Db	901	AATCAGTGGTGATCATTTGGGAATTTGTCGTCACCAATCTGTCCTCCCTGTTCTG	960	XX	14-NOV-2001; 2001US-00992598.		
Qy	961	ATATTGATCTGGAAGAGACCTGTGGAATAAGAGTTTCAGTGAATTCACAGTCTTTGGTG	1020	XX	97US-0049787P;	97US-0062250P.	
Db	961	ATATTGATCTGGAAGAGACCTGTGGAATAAGAGTTTCAGTGAATTCACAGTCTTTGGTG	1020	XX	97WO-US020069.	97US-0065311P.	
Qy	1021	AAGAACACGAGAGACTAATCCAGAGATAAAAGAAAACCTTGCCATTTTGAAGATGT	1080	XX	98US-0075945P.	98US-0078910P.	
Db	1021	AAGAACACGAGAGACTAATCCAGAGATAAAAGAAAACCTTGCCATTTTGAAGATGT	1080	XX	98US-0083322P.	98US-0083322P.	
Qy	1081	GAGGGGAGAAACACATTTACTCCCAATTAATGTACGGGAGTGATCGAGGAGAGAGAA	1140	XX	98US-0087106P.	98US-0087607P.	
Db	1081	GAGGGGAGAAACACATTTACTCCCAATTAATGTACGGGAGTGATCGAGGAGAGAGAA	1140	XX	98US-0087607P.	98US-0087759P.	
Qy	1141	CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCCTTCTCTGAGG	1200	XX	98US-0087827P.	98US-0088021P.	
Db	1141	CCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCCTTCTCTGAGG	1200	XX	98US-0088025P.	98US-0088026P.	
Qy	1201	TCAGATCGGAACAACTCACTTGAATAAAAGTCAAGTGGGGGATGCCAAAAACACAGCAA	1260	XX	98US-0088028P.	98US-0088029P.	
Db	1201	TCAGATCGGAACAACTCACTTGAATAAAAGTCAAGTGGGGGATGCCAAAAACACAGCAA	1260	XX	98US-0088033P.	98US-0088033P.	
Qy	1261	GCCTTTTGAAGAATCGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTG	1320	XX	98US-0088167P.	98US-0088202P.	
Db	1261	GCCTTTTGAAGAATCGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTG	1320	XX	98US-0088212P.	98US-0088217P.	
Qy	1321	TGTGTCTCTGGGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTGT	1380	XX	98US-0088655P.	98US-0088734P.	
Db	1321	TGTGTCTCTGGGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTGT	1380	XX	98US-0088738P.	98US-0088742P.	
Qy	1381	CTCATTTGTTGGTCAATACACTGAAGTGGAGATTTGGAGCCCTGGCAGAGACTGGAC	1440	XX	98US-0088810P.	98US-0088824P.	
Db	1381	CTCATTTGTTGGTCAATACACTGAAGTGGAGATTTGGAGCCCTGGCAGAGACTGGAC	1440	XX	98US-0088826P.	98US-0088858P.	
Qy	1441	AGCTCTCGAGAAACAGGCTCTCAGAGGAGGGAGCATGACATTTGGCTCTCGAGTGGG	1500	XX	98US-0088861P.	98US-0088876P.	
Db	1441	AGCTCTCGAGAAACAGGCTCTCAGAGGAGGGAGCATGACATTTGGCTCTCGAGTGGG	1500	XX	98US-0089105P.	98US-0089440P.	
Qy	1501	ACACTGGCCCTGGGAACCAAGCTGAGTGGCTCAAAACCCCGCTTGATCAGACC	1560	XX	98US-0089512P.	98US-0089514P.	

QY 781 ACTGTCAGTATCACCTAGGAACTGGTGTTCAGAGAAACCAATGCTGTCATGTCAGC 840
Db 781 ACCTGCAGTATCACCTAGGAACTGGTGTTCAGAGAAACCAATGCTGTCATGTCAGC 840
QY 841 CCGGAAGAGCTCGAATCTGGTGTACCCCGGAGCCCTGAGGCTCTGCTGCTGGTGGT 900
Db 841 CCGGAAGAGCTCGAATCTGGTGTACCCCGGAGCCCTGAGGCTCTGCTGCTGGTGGT 900
QY 901 AATCAGTGGTGTATCTATGTTGGAAATGCTGTGCCACAAATCTGCTGCTCCCTGTTCTG 960
Db 901 AATCAGTGGTGTATCTATGTTGGAAATGCTGTGCCACAAATCTGCTGCTCCCTGTTCTG 960
QY 961 ATATTGATCGTGAAGAGCTGCTGGAATTAAGAGTTGAGTGTCTACAGTCTTGGTG 1020
Db 961 ATATTGATCGTGAAGAGCTGCTGGAATTAAGAGTTGAGTGTCTACAGTCTTGGTG 1020
QY 1021 AAGAACACGAGAGAGCTATATCCAGAGATAAAAGAAAACCCCTGCCATTTTGAAGATGT 1080
Db 1021 AAGAACACGAGAGAGCTATATCCAGAGATAAAAGAAAACCCCTGCCATTTTGAAGATGT 1080
QY 1081 GAAGGGGAGAAACACATTTTACTCCCAATTAATTTGTACGGAGGTGATCGAGGAAGAGAA 1140
Db 1081 GAAGGGGAGAAACACATTTTACTCCCAATTAATTTGTACGGAGGTGATCGAGGAAGAGAA 1140
QY 1141 CCAAGTGAAAATCAGAGGCCACCTACATGACCAATGACCCAGTTTGGGCTTCTCTGAGG 1200
Db 1141 CCAAGTGAAAATCAGAGGCCACCTACATGACCAATGACCCAGTTTGGGCTTCTCTGAGG 1200
QY 1201 TCAGATCGGAACAACTCAGTTGAAAAGAGTCAAGTGGGGGAATGCCAAAACACAGCAA 1260
Db 1201 TCAGATCGGAACAACTCAGTTGAAAAGAGTCAAGTGGGGGAATGCCAAAACACAGCAA 1260
QY 1261 GCCTTTTGAAGAAATGAGAGTCCCTTCTATCTCAGCAGCGGTGGAGACTCTCTCTGTG 1320
Db 1261 GCCTTTTGAAGAAATGAGAGTCCCTTCTATCTCAGCAGCGGTGGAGACTCTCTCTGTG 1320
QY 1321 TGTGTCCTGGCCACTCTACAGTGTATTCAGACTCCCGCTCTCCAGCTGCTCTCTCTGT 1380
Db 1321 TGTGTCCTGGCCACTCTACAGTGTATTCAGACTCCCGCTCTCCAGCTGCTCTCTCTGT 1380
QY 1381 CTCATTTGTTGGTCAATACACTGAAGATGAGAAATTTGGAGCCTGGCAGAGAGACTGGAC 1440
Db 1381 CTCATTTGTTGGTCAATACACTGAAGATGAGAAATTTGGAGCCTGGCAGAGAGACTGGAC 1440
QY 1441 AGCTCTGGAGAAACAGCCCTGCTGAGGGAGGGAGATGAGCTTGGCCCTCTGAGTGGG 1500
Db 1441 AGCTCTGGAGAAACAGCCCTGCTGAGGGAGGGAGATGAGCTTGGCCCTCTGAGTGGG 1500
QY 1501 ACAGTGGCCCTGGAAACAGGCTGAGCTGAGTGGCCCTCAACCCCGTTGGATCAGACC 1560
Db 1501 ACAGTGGCCCTGGAAACAGGCTGAGTGGCCCTCAACCCCGTTGGATCAGACC 1560
QY 1561 CTCTGTGGGAGGGTTCTTAGTGGATGAGTTACTGGGAAGAAATCAGAGATAAAACCAA 1620
Db 1561 CTCTGTGGGAGGGTTCTTAGTGGATGAGTTACTGGGAAGAAATCAGAGATAAAACCAA 1620
QY 1621 CCCAAATCAA 1630
Db 1621 CCCAAATCAA 1630

RESULT 13

ACA66938 standard; cDNA; 1630 BP.

XX AC

XX AC

XX 23-JUN-2003 (first entry)

DE cDNA encoding human PRO polypeptide #98.

XX Human; PRO polypeptide; secreted and transmembrane protein;

XX Human; PRO polypeptide; secreted and transmembrane protein;

KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic;
KW gene; ss.

XX Homo sapiens.

XX US2003036635-A1.

XX 20-FEB-2003.

XX 28-AUG-2002; 2002US-00230163.

XX 25-JUL-2000; 2000US-0220638P.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI;

XX MPI; 2003-342045/32.

XX P-PSDB; ABU80836.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for the manufacture of a medicament for diagnosing or treating
XX tumor.

XX Claim 2; Fig 195; 314pp; English.

XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides and polynucleotides are useful for preparing a medicament
XX useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
XX useful in diagnostic assays for PRO, by detecting its expression in
XX specific cells, tissues or serum, and for affinity purification of PRO
XX from recombinant cell culture or natural sources. ACA66841-ACA66962
XX represent cDNA sequences encoding the human PRO polypeptides of the
XX invention. Note: the sequence data for this patent was obtained in
XX electronic format directly from the USPTO web site at
XX seqdata.uspto.gov/psipdsIDEntry.html

XX Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 1630; DB 7; Length 1630;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTGAGTGCAGCTGTGGGAGATTTTCAGTGCATTGCTCCCTCCCTGGGTGCTTTCATC 60

Db 1 CGGCTGAGTGCAGCTGTGGGAGATTTTCAGTGCATTGCTCCCTCCCTGGGTGCTTTCATC 60

QY 61 TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCCACTGAAACTCACTGCTGCCAGTG 120

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Db 121 TTACTGATTTATTCCTTGGCCCTGATGACTTGAATGTTTCCCGCTGGCTAAGATC 180

QY 181 CATGTGGTGTATTCAGCTCTGATGGGATGTTTCCAGAGCAGAGAAACAATGTATA 240

Db 181 CATGTGGTGTATTCAGCTCTGATGGGATGTTTCCAGAGCAGAGAAACAATGTATA 240

QY 241 TTCAAGATAGACTGGACTCTGTCCAGGAGAGACGCCAAGGACGAATATGCTATAC 300

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QY 421 ACCTATATCTGTGAATTCGCGCTCAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTTGGTA 480
Db 421 ACCTATATCTGTGAATTCGCGCTCAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTTGGTA 480
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QY 1621 CCCAAATCAA 1630
Db 1621 CCCAAATCAA 1630
RESULT 14
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ID ACD68690 standard; cDNA; 1630 BP.
XX
AC ACD68690;
XX
DT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1387 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
KW arthritis; wound; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003045687-A1.
XX
PD 06-MAR-2003.
XX
PF 12-AUG-2002; 2002US-00218631.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-512315/48.
DR P-PSDB; ABO33802.
XX
PT New genes, and its encoded secreted and transmembrane polypeptides,
PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
PT pericyte proliferation, especially for treating lung tumors, arthritis or
PT wounds in a mammal.
XX
PS Claim 2; Fig 195; 314pp; English.
XX
CC The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
CC fully defined in the specification; or (b) any of 122 nucleotide
CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte

cells, for stimulating proliferation of pericyte cells, or for modulating normal human fibroblast proliferation. The PRO nucleic acid or polypeptide is also useful for treating tumours or various bone and/or cartilage disorders (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This sequence encodes a novel human secreted and transmembrane PRO polypeptide.

Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;

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Qy	361	GACATCTTATGCAATGATGGCTCTCTCTGCTCAGATGTGCGAAGAGCTGACACAGGA	420
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XX OS Homo sapiens.
XX PN US2002103125-A1.
XX PD 01-AUG-2002.
XX PF 20-NOV-2001; 2001US-00989731.
XX PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075845P.
PR 28-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
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PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
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PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
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PR 05-JUN-1998; 98US-0088212P.
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PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
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PR 17-JUN-1998; 98US-0089532P.
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PR 18-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019337.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.

XX PA (GETH ) GENENTECH LTD.
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX WPI; 2003-102117/09.
XX DR P-PSDB; ABU13993.
XX PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX Claim 2; Fig 303; 649pp; English.
XX CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides, for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. The present
CC sequence encodes a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/psipsIDentry.html
XX CC
XX CC Sequence 1630 BP; 425 A; 369 C; 452 G; 384 T; 0 U; 0 Other;
XX CC
XX CC Query Match 100.0%; Score 1630; DB 7; Length 1630;
XX CC Best Local Similarity 100.0%; Pred. No. 0;
XX CC Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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and is derived by analysis of the total score distribution.

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2	1534.8	94.2	1561	4	US-09-656-952-18
3	1494.8	91.7	1591	4	US-09-656-952-17
4	1483.8	91.0	1592	4	US-09-656-952-1
5	1194.4	73.3	1207	4	US-08-023-655-131
6	609.8	37.4	1024	2	US-08-867-680-1
7	485.6	29.8	1158	4	US-09-663-600A-50
8	485.6	29.8	1158	4	US-09-663-600A-144
9	51.6	3.2	7218	1	US-08-232-463-14
10	40.6	2.5	438	4	US-09-702-705-1549
11	40.6	2.5	438	4	US-09-736-457-1549
12	40.6	2.5	438	4	US-09-614-124B-1549
13	40.6	2.5	438	4	US-09-671-325-1549
14	40.6	2.5	1871	1	US-08-416-478A-1
15	40.6	2.5	1871	2	US-08-474-988B-1
16	40.6	2.5	1871	2	US-08-394-442B-1
17	38.4	2.4	1602	4	US-09-672-434-1
18	38.4	2.4	7872	4	US-09-956-171E-161
19	37	2.3	385	4	US-09-621-976-19314
20	37	2.3	489	4	US-09-621-976-19303
21	35.4	2.2	1275	1	US-08-588-113-1
22	35	2.1	505	4	US-09-621-976-15639
23	35	2.1	1608	4	US-09-134-001C-2407
24	34.6	2.1	526	4	US-09-621-976-16411
25	34.4	2.1	832	4	US-09-621-976-2813
26	34.4	2.1	1073	4	US-09-430-503-25
27	34.4	2.1	1073	4	US-09-430-503-27

28	34.4	2.1	1073	4	US-09-430-503-29	Sequence 29, Appli
29	34.4	2.1	1073	4	US-09-430-503-31	Sequence 31, Appli
30	34.4	2.1	1584	3	US-08-928-383B-1	Sequence 1, Appli
31	34.4	2.1	2434	3	US-09-272-496-1	Sequence 1, Appli
32	34.2	2.1	1489	4	US-09-976-594-730	Sequence 730, App
33	34	2.1	495	4	US-09-134-001C-1793	Sequence 1793, Ap
34	34	2.1	5181	1	US-08-257-073-10	Sequence 10, Appli
35	34	2.1	21784	4	US-08-820-002-3	Sequence 3, Appli
36	33.8	2.1	1164	1	US-08-416-478A-5	Sequence 5, Appli
37	33.8	2.1	1164	2	US-08-474-988B-5	Sequence 5, Appli
38	33.8	2.1	1164	2	US-08-394-442B-5	Sequence 5, Appli
39	33.8	2.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
40	33.6	2.1	1983	1	US-08-073-799C-9	Sequence 9, Appli
41	33.4	2.0	7052	4	US-08-526-193A-22	Sequence 22, Appli
42	33	2.0	6426	4	US-09-976-594-136	Sequence 136, App
43	32.8	2.0	1060	4	US-08-937-685A-7	Sequence 7, Appli
44	32.8	2.0	1597	3	US-09-038-832-3	Sequence 3, Appli
45	32.8	2.0	1656	4	US-09-446-301A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-855-323-11
; Sequence 11, Application US/09855323
; Patent No. 6602667
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: Inflammation-Associated Polynucleotides
; FILE REFERENCE: PB-0006-1 CIP
; CURRENT APPLICATION NUMBER: US/09/855,323
; CURRENT FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 1751
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 3507924CB1
US-09-855-323-11

Query Match 99.5%; Score 1621.4; DB 4; Length 1751;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1622; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	7	GAGTGCAGCTGTGGGAGATTTCAGTCGATTCGCTCCCTGGGTCTTTCATCTGGAT	66
Db	108	GACTGCAGCTGTGGGAGATTTCAGTCGATTCGCTCCCTGGGTCTTTCATCTGGAT	167
Qy	67	TTGAAAGTTGAGACGACGATGTTTGGCCACTGAAATTCATCTCCCTGCGCAGTGTACTG	126
Db	168	TTGAAAGTTGAGACGACGATGTTTGGCCACTGAAATTCATCTCCCTGCGCAGTGTACTG	227
Qy	127	GATTATTCCTTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATGTG	186
Db	228	GATTATTCCTTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATGTG	287
Qy	187	GGTGATTCAGCTCTGATGGATGTTTCCAGAGCAGACAGCAATATGTATTTCAAG	246
Db	288	GGTGATTCAGCTCTGATGGATGTTTCCAGAGCAGACAGCAATATGTATTTCAAG	347
Qy	247	ATAGACTGGACTCTGTCCAGGAGACGACGCCAAGGACGAATATGTCTATATTATAC	306
Db	348	ATAGACTGGACTCTGTCCAGGAGACGACGCCAAGGACGAATATGTCTATATTATAC	407
Qy	307	TCCAATCTCAGTGTGCTTATTTGGGCGCTTCCAGAACCGGTACACTTGTATGGGGACATC	366
Db	408	TCCAATCTCAGTGTGCTTATTTGGGCGCTTCCAGAACCGGTACACTTGTATGGGGACATC	467

QY 367 TTATGCAATGATGGCTCTCTCTCTCAAGATGTGCAAGGCTGACACAGGACCTAT 426
Db 468 TTATGCAATGATGGCTCTCTCTCTCAAGATGTGCAAGGCTGACACAGGACCTAT 527
QY 427 ATCTGTGAATCCGCTCTCAAGGGGAGAGCCAGAGTGTTCAGAGAGCGGTGTCTGCAAT 486
Db 528 ATCTGTGAATCCGCTCTCAAGGGGAGAGCCAGAGTGTTCAGAGAGCGGTGTCTGCAAT 587
QY 487 GTGCTTCAGAGAGCCCAAGAGCTCATGTGTCATGTGGGTGGATGTGATTCAGATGGGA 546
Db 588 GTGCTTCAGAGAGCCCAAGAGCTCATGTGTCATGTGGGTGGATGTGATTCAGATGGGA 647
QY 547 TGTGTTTTCCAGAGCACAGAGTGAACACAGTGAACCAAGGTAGATGATATTTTCAGGA 606
Db 648 TGTGTTTTCCAGAGCACAGAGTGAACACAGTGAACCAAGGTAGATGATATTTTCAGGA 707
QY 607 CGGCGCGCAAGGAGGAGATTGTATTTCTGTACTACCAAACTCAGGATGTCTGTGGAG 666
Db 708 CGGCGCGCAAGGAGGAGATTGTATTTCTGTACTACCAAACTCAGGATGTCTGTGGAG 767
QY 667 TACTCCAGAGCTGGGGCCACTTCAGAACTGTGTGAACCTGGTGGGGACATTTTCGCG 726
Db 768 TACTCCAGAGCTGGGGCCACTTCAGAACTGTGTGAACCTGGTGGGGACATTTTCGCG 827
QY 727 AATGACGGTTCATCATGCTTCAAGAGTGAAGGAGTCAGATGGAGGAACTACACCTGC 786
Db 828 AATGACGGTTCATCATGCTTCAAGAGTGAAGGAGTCAGATGGAGGAACTACACCTGC 887
QY 787 AGTATCCACTAGGGAACCTGGTGTCAAGAAACCATTTGTCTGCATGTCTGATCGCCGAA 846
Db 888 AGTATCCACTAGGGAACCTGGTGTCAAGAAACCATTTGTCTGCATGTCTGATCGCCGAA 947
QY 847 GAGCTCCAAACACTGGTCAACCCGAGCCCTGAGGCTCTGGTCTTGGGTGTAATCAG 906
Db 948 GAGCTCCAAACACTGGTCAACCCGAGCCCTGAGGCTCTGGTCTTGGGTGTAATCAG 1007
QY 907 TTGTGTGATCAATGTGGGAATGTCTGTGCCAAATCTCTGCTCCCTGTTCTGATATTG 966
Db 1008 TTGTGTGATCAATGTGGGAATGTCTGTGCCAAATCTCTGCTCCCTGTTCTGATATTG 1067
QY 967 ATCTGTGAAGAGACTGTGTGGAATTAAGAGTTCAAGTAATTTACAGTCTTGGTGAAGAAC 1026
Db 1068 ATCTGTGAAGAGACTGTGTGGAATTAAGAGTTCAAGTAATTTACAGTCTTGGTGAAGAAC 1127
QY 1027 ACGAAGAGACTAATCCAGAGATAAAGAAACCTGCCATTTTGAAGATGTGAAGG 1086
Db 1128 ACGAAGAGACTAATCCAGAGATAAAGAAACCTGCCATTTTGAAGATGTGAAGG 1187
QY 1087 GAGAAACACATTTACTCCCCCAATTAATGTACGGGAGGTGATCGAGGAAGAAACCAAGT 1146
Db 1188 GAGAAACACATTTACTCCCCCAATTAATGTACGGGAGGTGATCGAGGAAGAAACCAAGT 1247
QY 1147 GAAAAATCAGAGGCCACCTACATGACCAATGACCCAGTTTGGCTTCTCTGAGGTGAGT 1206
Db 1248 GAAAAATCAGAGGCCACCTACATGACCAATGACCCAGTTTGGCTTCTCTGAGGTGAGT 1307
QY 1207 CGGAACACTCACTTGAAAGAGTCAAGTGGGGGAATGCCAAACACAGCAAGCCCTTT 1266
Db 1308 CGGAACACTCACTTGAAAGAGTCAAGTGGGGGAATGCCAAACACAGCAAGCCCTTT 1367
QY 1267 TGAGAAGATGGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTGTGTGTC 1326
Db 1368 TGAGAAGATGGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTGTGTGTC 1427
QY 1327 CTGGGCCACTTACAGTGAATTCAGACTCCGGCTCTCCAGCTGTCTCTCTGTCTCATTT 1386
Db 1428 CTGGGCCACTTACAGTGAATTCAGACTCCGGCTCTCCAGCTGTCTCTCTGTCTCATTT 1487
QY 1387 GTTTCGTCAATACACTGAAGATGGAGAAATTTGAGCCTGGCAGAGAGACTTGACAGCTCT 1446
Db 1488 GTTTCGTCAATACACTGAAGATGGAGAAATTTGAGCCTGGCAGAGAGACTTGACAGCTCT 1547
QY 1447 GGAGGAACAGGCTCTCTGAGGGGAGGGAGCATGGACTTTGGCCTCTGGAGTGGGACACTG 1506

Db 1548 GGAGGAACAGGCTCTCTGAGGGGAGGAGCATGACTTTGGCTCTGGAGTGGGACACTG 1607
QY 1507 GCCCTGGAAACAGGCTGAGCTGAGTGGCTCAAAACCCCGCTTGGATCAGACCTCTCTG 1566
Db 1608 GCCCTGGAAACAGGCTGAGCTGAGTGGCTCAAAACCCCGCTTGGATCAGACCTCTCTG 1667
QY 1567 TGGGACAGGTTCTTAGTGGATGAGTTACTGGGAGAAATCAGAGATAAAACCAACCCAAA 1626
Db 1668 TGGGACAGGTTCTTAGTGGATGAGTTACTGGGAGAAATCAGAGATAAAACCAACCCAAA 1727
QY 1627 TCA 1629
Db 1728 TCA 1730

RESULT 2
US-09-656-952-18
; Sequence 18, Application US/09656952
; Patent No. 6444443
; GENERAL INFORMATION:
; APPLICANT: Gabor Jarai et al.
; TITLE OF INVENTION: No. 644443el Gene
; FILE REFERENCE: 4-31440PI/NI/HO 29
; CURRENT APPLICATION NUMBER: US/09/656,952
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 1561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-656-952-18

Query Match 94.2%; Score 1534.8; DB 4; Length 1561;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 44 CCTGGTGCTCTTCATCTTGAATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAC 103
Db 2 CCTTTGCTCTTCATCTTGAATTTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAC 61
QY 104 TCATCCTCTGCCAGTGTACTGTGATTTCTTGGGCTGAACTGACTTGAATGTTTCCC 163
Db 62 TCATCCTCTGCCAGTGTACTGTGATTTCTTGGGCTGAACTGACTTGAATGTTTCCC 121
QY 164 CGCTGAGCTAACAGTCCATGTGGTGAATCAGCTCTGATGGATGTGTTCAGAGCA 223
Db 122 CGCTGAGCTAACAGTCCATGTGGTGAATCAGCTCTGATGGATGTGTTCAGAGCA 181
QY 224 CAGAGACAAATGTATTTCAAGATAGACTGACTCTGTCCAGGAGGAGCAGCCAGG 283
Db 182 CAGAGACAAATGTATTTCAAGATAGACTGACTCTGTCCAGGAGGAGCAGCCAGG 241
QY 284 ACGAATATGTGTATCTACTTACTTCAATCTCAGTGTGCTTATTTGGGCGCTTCCAGAAC 343
Db 242 ACGAATATGTGTATCTACTTACTTCAATCTCAGTGTGCTTATTTGGGCGCTTCCAGAAC 301
QY 344 CGGTACACTTGAATGGGGACATCTTATGCAATGATGGTCTCTCTCTGTCGAAGATGTGC 403
Db 302 CGGTACACTTGAATGGGGACATCTTATGCAATGATGGTCTCTCTCTGTCGAAGATGTGC 361
QY 404 AAGAGCTGACCCAGGAACTTATCTGTGAATCCGCTCAAGGGGAGGAGCCAGGTGT 463
Db 362 AAGAGCTGACCCAGGAACTTATCTGTGAATCCGCTCAAGGGGAGGAGCCAGGTGT 421
QY 464 TCAAGAGAGCGGTGTGTACTGTGATGTCTTCCAGAGGAGCCCAAGAGCTCATGTCTCATG 523
Db 422 TCAGAGAGCGGTGTGTACTGTGATGTCTTCCAGAGGAGCCCAAGAGCTCATGTCTCATG 481
QY 524 TGGGTGATTTGATTCAGATGGGATGTGTTTCCAGAGCAGAGAGTGAACACGTGACCA 583
Db 482 TGGGTGATTTGATTCAGATGGGATGTGTTTCCAGAGCAGAGAGTGAACACGTGACCA 541

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QY 584 AGGTAGATGATATTTTCAGACGGCGCGCAAGGAGGAGATTGTATTTGTTACTACC 643
Db 542 AGGTAGATGATATTTTCAGACGGCGCGCAAGGAGGAGATTGTATTTGTTACTACC 601
QY 644 ACAAACTCAGGATGCTGTGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGGA 703
Db 602 ACAAACTCAGGATGCTGTGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGGA 661
QY 704 ACCTGGTGGGACATTTTCGCAATGACGGTTCATCATCTTCAAGAGTGAGGGAGT 763
Db 662 ACCTGGTGGGACATTTTCGCAATGACGGTTCATCATCTTCAAGAGTGAGGGAGT 721
QY 764 CAGATGGAGGAACATACACCTGCAGTATCCACCTAGGGAACCTGGTGTCAAGAAACCA 823
Db 722 CAGATGGAGGAACATACACCTGCAGTATCCACCTAGGGAACCTGGTGTCAAGAAACCA 781
QY 824 TTGTGCTCATGTGACCCCGGAAGAGCTCGAAACACTGGTGACCCCGCAGCCCTGAGGC 883
Db 782 TTGTGCTCATGTGACCCCGGAAGAGCTCGAAACACTGGTGACCCCGCAGCCCTGAGGC 841
QY 884 CTCTGGTCTTGGGTGGTAATCAGTTGGTGATCAATTTGGGGAATTTCTGTGCCAATACC 943
Db 842 CTCTGGTCTTGGGTGGTAATCAGTTGGTGATCAATTTGGGGAATTTCTGTGCCAATACC 901
QY 944 TGCTGCTCCCTGTTCTGATATTTGATCGTGAAGAGACCTGTGGAAATGAAGATTTCAGTA 1003
Db 902 TGCTGCTCCCTGTTCTGATATTTGATCGTGAAGAGACCTGTGGAAATGAAGATTTCAGTA 961
QY 1004 ATTCTACAGTCTTGGTGAAGAACACGAAGAGACTTAATCCAGAGATAAAGAAACCCCT 1063
Db 962 ATTCTACAGTCTTGGTGAAGAACACGAAGAGACTTAATCCAGAGATAAAGAAACCCCT 1021
QY 1064 GCCATTTTGAAGATGTGAAGGGGAGAAACAAATTTACTCCCAATAATTTGACGGGAGG 1123
Db 1022 GCCATTTTGAAGATGTGAAGGGGAGAAACAAATTTACTCCCAATAATTTGACGGGAGG 1081
QY 1124 TGATCGAGGAGAGAACCAAGTGAAGAAATCAGAGGCCACCTACATGACCATGCACCAG 1183
Db 1082 TGATCGAGGAGAGAAACCAAGTGAAGAAATCAGAGGCCACCTACATGACCATGCACCAG 1141
QY 1184 TTGGCCCTTCTCTGAGGTGAGTCCGAACAACTCACTTTGAAAAAAGTCAGTGGGGGAA 1243
Db 1142 TTGGCCCTTCTCTGAGGTGAGTCCGAACAACTCACTTTGAAAAAAGTCAGTGGGGGAA 1201
QY 1244 TGCMAAAACACAGCAAGCCTTTTGAGAAAGATGGAGAGTCCCTTCATCTCAGCAGCGGT 1303
Db 1202 TGCMAAAACACAGCAAGCCTTTTGAGAAAGATGGAGAGTCCCTTCATCTCAGCAGCGGT 1261
QY 1304 GGAGACTCTCTCCTGTGTGTCCTGGGCGCACTCTACAGTGATTTTCAGACTCCCGCTCT 1363
Db 1262 GGAGACTCTCTCCTGTGTGTCCTGGGCGCACTCTACAGTGATTTTCAGACTCCCGCTCT 1321
QY 1364 CCCAGCTCTCCTGTCTCATTTGTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCC 1423
Db 1322 CCCAGCTCTCCTGTCTCATTTGTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCC 1381
QY 1424 TGGCAGAGAGACTGACAGCTCTTGAGGAAACAGGCCCTCTGAGGGGAGGGAGCATGAC 1483
Db 1382 TGGCAGAGAGACTGACAGCTCTTGAGGAAACAGGCCCTCTGAGGGGAGGGAGCATGAC 1440
QY 1484 TTGGCCTCTGGAGTGGGACACTGGCCCTGGGAAACAGGCTGAGTGGGCTCAACACC 1543
Db 1441 TTGGCCTCTGGAGTGGGACACTGGCCCTGGGAAACAGGCTGAGTGGGCTCAACACC 1500
QY 1544 CCCCGTTGGATCAGACCTCTCTGTGGGAGGGTTCTTAGTGGATGAGTTACTTGGGAAG 1601
Db 1501 CCCCGTTGGATCAGACCTCTCTGTGGGAGGGTTCTTAGTGGATGAGTTACTTGGGAAG 1558
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RESULT 3

US-09-656-952-17

; Sequence 17, Application US/09656952

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; Patent No. 6444443
; GENERAL INFORMATION:
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; APPLICANT: Gabor Jarai et al.
; TITLE OF INVENTION: No. 644443el Gene
; FILE REFERENCE: 4-31440P1/N1/HO 29
; CURRENT APPLICATION NUMBER: US/09/656,952
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 1591
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-656-952-17
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Query Match 91.7%; Score 1494.8; DB 4; Length 1591;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 7; Indels 31; Gaps 2;
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QY 44 CTGGGTGCTCTTTCATCTTGAAGTTGAGAGCAGCATGTTTGGCCACTGAAC 103
Db 2 CCCTTGCTCTTTCATCTTGAAGTTGAGAGCAGCATGTTTGGCCACTGAAC 61
QY 104 TCATCCTGCTGCCAGTGTACTGATTAATTCCTTGGGCTGAATGACTTGAATGTTCCC 163
Db 62 TCATCCTGCTGCCAGTGTACTGATTAATTCCTTGGGCTGAATGACTTGAATGTTCCC 121
QY 164 CGCTGAGCTAACAGTCCATGTGGTGATTCAGTCTGTGATGGGATGTTTTCCAGACA 223
Db 122 CGCTGAGCTAACAGTCCATGTGGTGATTCAGTCTGTGATGGGATGTTTTCCAGACA 181
QY 224 CAGAGCAAAATGATATTCAGATAGACTGACTCTGTCCACGAGGAGACGCCAAGG 283
Db 182 CAGAGCAAAATGATATTCAGATAGACTGACTCTGTCCACGAGGAGACGCCAAGG 241
QY 284 ACGAATATGTCTATTAATTTACTCCAACTCAGTGTGCTCTATTTGGGGCTTCCAGAAC 343
Db 242 ACGAATATGTCTATTAATTTACTCCAACTCAGTGTGCTCTATTTGGGGCTTCCAGAAC 301
QY 344 CGGTACACTTGAATGGGGACATCTTATGCAATGATGGCTCTCTCTCTGCTCCAAGATGTC 403
Db 302 CGGTACACTTGAATGGGGACATCTTATGCAATGATGGCTCTCTCTCTGCTCCAAGATGTC 361
QY 404 AAGAGGCTGACACAGGAACCTATATCTGTGAATCCGCTCAAGGGGAGAGCCAGTGT 463
Db 362 AAGAGGCTGACACAGGAACCTATATCTGTGAATCCGCTCAAGGGGAGAGCCAGTGT 421
QY 464 TCAAGAGCGCGTGGTACTGCTGCTTCCAGAGAGGCCCAAGAGCTCATGTGCCATG 523
Db 422 TCAGAGAGCGCGTGGTACTGCTGCTTCCAGAGAGGCCCAAGAGCTCATGTGCCATG 481
QY 524 TGGGTGGAATGAATCAGATGGGATGTTTTTCCAGAGACAGAAAGTGAACACGTTGACA 583
Db 482 TGGGTGGAATGAATCAGATGGGATGTTTTTCCAGAGACAGAAAGTGAACACGTTGACA 541
QY 584 AGGTAGATGATATTTTCAGACGGCGCGCAAGGAGGAGATTGTATTTGTTACTACC 643
Db 542 AGGTAGATGATATTTTCAGACGGCGCGCAAGGAGGAGATTGTATTTGTTACTACC 601
QY 644 ACAAACTCAGGATGCTGTGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGGA 703
Db 602 ACAAACTCAGGATGCTGTGAGTACTCCAGAGCTGGGGCCACTTCCAGAAATCGTGGA 661
QY 704 ACCTGGTGGGGAACATTTTCGCAATGACGGTTCATCATCTTCAAGAGTGAGGGAGT 763
Db 662 ACCTGGTGGGGAACATTTTCGCAATGACGGTTCATCATCTTCAAGAGTGAGGGAGT 721
QY 764 CAGATGGAGGAACATACACCTGCAGTATCCACCTAGGGAACCTGGTGTCAAGAAACCA 823
Db 722 CAGATGGAGGAACATACACCTGCAGTATCCACCTAGGGAACCTGGTGTCAAGAAACCA 781
QY 824 TTGTGCTCATGTGACCCCGGAAGAGCTCGAAACACTGGTGACCCCGCAGCCCTGAGGC 883
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Db 1022 TGCCATTTTGAAGAGTGTGAAGGGAGGTGAACACACAGCTTCAGCCTAAACACATAAAA 1081
Qy 1093 CACATTACTCCCAATTAATGTACGGGAGGTGATCAGGAAGAAACCAAGTGA AAAA 1152
Db 1082 CACATTACTCCCAATTAATGTACGGGAGGTGATCAGGAAGAAACCAAGTGA AAAA 1141
Qy 1153 TCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCCTTCTCTGAGGTGATCGGAAC 1212
Db 1142 TCAGAGGCCACCTACATGACCATGACCCAGTTTGGCCCTTCTCTGAGGTGATCGGAAC 1201
Qy 1213 AACTCACTTGA AAAAAGTCAAGTGGGGAAATGCCAAAAACACAGCAAGCTTTTGA AAA 1272
Db 1202 AACTCACTTGA AAAAAGTCAAGTGGGGAAATGCCAAAAACACAGCAAGCTTTTGA AAA 1261
Qy 1273 GAATGAGAGTCCCTTCATCTCAGACGCGGTGAGACTCTCTCTGTGTGTCTGTTGG 1332
Db 1262 GAATGAGAGTCCCTTCATCTCAGACGCGGTGAGACTCTCTCTGTGTGTCTGTTGG 1321
Qy 1333 CACTCTACCAAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTGTGTGTCTGTTGG 1392
Db 1322 CACTCTACCAAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTGTGTGTCTGTTGG 1381
Qy 1393 TCAATACACTGAAGATGGAGAAATTTGGAGCTTGGCAGAGAGACTGACAGCTCTGAGGA 1452
Db 1382 TCAATACACTGAAGATGGAGAAATTTGGAGCTTGGCAGAGAGACTGACAG-TC TGAAGA 1440
Qy 1453 ACAGGCGCTCTGAGGGGAGGAGCATGACTTGGCTCTGAGTGGGACACTGGCCCTG 1512
Db 1441 ACAGGCGCTCTGAGGGGAGGAGCATGACTTGGCTCTGAGTGGGACACTGGCCCTG 1500
Qy 1513 GGAACAGGCTGAGTGTGAGTGGCTCAAAACCCCGTTGATCAGACCCCTCTGTGGCA 1572
Db 1501 GGAACAGGCTGAGTGTGAGTGGCTCAAAACCCCGTTGATCAGACCCCTCTGTGGCA 1560
Qy 1573 GGGTTCTTAGTGGATGAGTACTGGGAAG 1601
Db 1561 GGGTTCTTAGTGGATGAGTACTGGGAAG 1589

RESULT 5

US-09-023-655-131

; Sequence 131, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SPLNFT01
; CLONE: 027756
; US-09-023-655-131

Query Match 73.3%; Score 1194.4; DB 4; Length 1207;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 434 AAATCGCCCTCAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTGCTACTGCTGCTTC 493
Db 1 AAATCGCCCTCAAGGGGAGAGCCAGGTGTTCAAGAAAGCGGTGCTACTGCTGCTTC 60
Qy 494 CAGAGAGCCCAAGAGAGCTCATGTCCTCATGTCGGTGGATTGATTGAGATGGGATGTTT 553
Db 61 CAGAGAGCCCAAGAGAGCTCATGTCCTCATGTCGGTGGATTGATTGAGATGGGATGTTT 120
Qy 554 TCCAGAGCACAGAAAGTGAACACACGTGACCAAGTGAAGATGGATATTTTCAGGACGCGCG 613
Db 121 TCCAGAGCACAGAAAGTGAACACACGTGACCAAGTGAAGATGGATATTTTCAGGACGCGCG 180
Qy 614 CAAAGAGGAGATTTGATTTTCTTACTACCAAACTCAGGATGTCGTGGAGTACTCC 673
Db 181 CAAAGAGGAGATTTGATTTTCTTACTACCAAACTCAGGATGTCGTGGAGTACTCC 240
Qy 674 AGAGCTGGGGCCACTTCCAGATCTGTGAACCTCGTGGGGACATTTTCCCAATGAG 733
Db 241 AGAGCTGGGGCCACTTCCAGATCTGTGAACCTCGTGGGGACATTTTCCCAATGAG 300
Qy 734 GTTCCATCATGCTTCAAGGAGTGAGGGAGTCAAGTGGAGGAACTACACTGCAGTATCC 793
Db 301 GTTCCATCATGCTTCAAGGAGTGAGGGAGTCAAGTGGAGGAACTACACTGCAGTATCC 360
Qy 794 ACCTAGGGAACCTGTGTTTCAAGAAACCATTTGCTGCTGATGTCAGCCCGGAGAGCCTC 853
Db 361 ACCTAGGGAACCTGTGTTTCAAGAAACCATTTGCTGCTGATGTCAGCCCGGAGAGCCTC 420
Qy 854 GAACACTGGTGACCCGCGACCCCTGAGCCTCTGCTTGGGTGGTAAATCAGTTGGTGA 913
Db 421 GAACACTGGTGACCCGCGACCCCTGAGCCTCTGCTTGGGTGGTAAATCAGTTGGTGA 480
Qy 914 TCATTGTGGGAATTTGCTGTGCCAATCCTGCTCTCTGCTCTGATTAATGATCGTGA 973
Db 481 TCATTGTGGGAATTTGCTGTGCCAATCCTGCTCTCTGCTCTGATTAATGATCGTGA 540
Qy 974 AGAAGACCTGTGGAATAAAGAGTTCAAGTGAATTTTACAGTCTTGTGTGAAGAACACGAAGA 1033
Db 541 AGAAGACCTGTGGAATAAAGAGTTCAAGTGAATTTTACAGTCTTGTGTGAAGAACACGAAGA 600
Qy 1034 AGACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGTCGAAGGGGAAAC 1093
Db 601 AGACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGTCGAAGGGGAAAC 660
Qy 1094 ACATTACTCCCAATTAATTTGAGGGAGGTGATCGAGGAAGAAACCAAGTGA AAAAT 1153
Db 661 ACATTACTCCCAATTAATTTGAGGGAGGTGATCGAGGAAGAAACCAAGTGA AAAAT 720
Qy 1154 CAGAGGCCACCTACATGACCAATGACCCAGTTTGGCCTTCTCTGAGGTGATCGGAACA 1213
Db 721 CAGAGGCCACCTACATGACCAATGACCCAGTTTGGCCTTCTCTGAGGTGATCGGAACA 780
Qy 1214 ACTCACTTGA AAAAAGTCAAGTGGGGGAATGCCAAAAACACAGCAAGCCTTTTGAAGA 1273

Db 781 ACTCACTGAAAAAAGTCAGGTGGGGAAATGCCAAAAACACAGACAGCTTTTGAAG 840
QY 1274 AATGAGAGTCCCTTCATCTCAGACGCGTGGAGACTCTCTCTGTGTGTCTGTGGCC 1333
Db 841 AATGAGAGTCCCTTCATCTCAGACGCGTGGAGACTCTCTCTGTGTGTCTGTGGCC 900
QY 1334 ACTTACAGTGTATTCAGACTCCGCTCTCCAGCTGTCCCTCTCTCTCTCTCTCTCT 1393
Db 901 ACTTACAGTGTATTCAGACTCCGCTCTCCAGCTGTCCCTCTCTCTCTCTCTCTCT 960
QY 1394 CAATACACTGAAGATGGAGAAATTTGAGGCTTGGCAGAGAGACTGGACAGCTCTGGAGAA 1453
Db 961 CAATACACTGAAGATGGAGAAATTTGAGGCTTGGCAGAGAGACTGGACAGCTCTGGAGAA 1020
QY 1454 CAGGCTGTCTGAGGGAGGGAGCATGGAATTTGGAGCTTGGCAGAGAGACTGGACAGCTCTGGAGAA 1513
Db 1021 CAGGCTGTCTGAGGGAGGGAGCATGGAATTTGGAGCTTGGCAGAGAGACTGGACAGCTCTGGAGAA 1080
QY 1514 GAACAGGCTGAGCTCAGTGGGCTCAAAACCCCGTTGGATCAGACCTCTCTGTGGGAG 1573
Db 1081 GAACAGGCTGAGCTCAGTGGGCTCAAAACCCCGTTGGATCAGACCTCTCTGTGGGAG 1140
QY 1574 GGTCTTCTAGTGGATGAGTTACTGGGAGAAATCAGAGATAAAACCAACCAATCA 1629
Db 1141 GGTCTTCTAGTGGATGAGTTACTGGGAGAAATCAGAGATAAAACCAACCAATCA 1196

RESULT 6

US-08-867-680-1
; Sequence 1, Application US/08867680
; Patent No. 5958726
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Racie, Lisa A.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Evans, Cheryl
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,680
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: P-41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1024 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-867-680-1

Query Match 37.4%; Score 609.8; DB 2; Length 1024;
Best Local Similarity 99.7%; Pred. No. 1.3e-194;
Matches 611; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7 GAGTGCAGCTGTGGGAGATTTTCAGTGCATTCCTCCCTCCCTGGTGTCTTCTTCTTGGAT 66
Db 2 GACTGCAGCTGTGGGAGATTTTCAGTGCATTCCTCCCTCCCTGGTGTCTTCTTCTTGGAT 61
QY 67 TTGAAGTTGAGAGAGCATGTTTGGCCACTGAAACTCATCTCTGCTGCGAGTTTACTG 126
Db 62 TTGAAGTTGAGAGAGCATGTTTGGCCACTGAAACTCATCTCTGCTGCGAGTTTACTG 121
QY 127 GATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGTAACTGATCCATGTTG 186
Db 122 GATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGTAACTGATCCATGTTG 181
QY 187 GGTGATTTCAGCTCTGATGGATGTGTTTCCAGAGACAGACAAATGATATTTCAAG 246
Db 182 GGTGATTTCAGCTCTGATGGATGTGTTTCCAGAGACAGACAAATGATATTTCAAG 241
QY 247 ATAGACTGCACTCTGTCCAGAGAGACGCGCAAGGAGAAATATGCTTACTATTAC 306
Db 242 ATAGACTGCACTCTGTCCAGAGAGACGCGCAAGGAGAAATATGCTTACTATTAC 301
QY 307 TCCAAATCTCAGTGTGCTTATTTGGGCGCTTCCAGAACCGGTACACTTTGATGGGGACATC 366
Db 302 TCCAAATCTCAGTGTGCTTATTTGGGCGCTTCCAGAACCGGTACACTTTGATGGGGACATC 361
QY 367 TTATGCAATGATGGCTCTCTCTGCTTCAAGATGTGCAAGAGGCTGACCAAGGAACTTAT 426
Db 362 TTATGCAATGATGGCTCTCTCTGCTTCAAGATGTGCAAGAGGCTGACCAAGGAACTTAT 421
QY 427 ATCTGTGAATCGGCTCAAGGGAGAGCCAGGTGTTTCAAGAGCGGTGTTGATTCAGATGGGA 546
Db 422 ATCTGTGAATCGGCTCAAGGGAGAGCCAGGTGTTTCAAGAGCGGTGTTGATTCAGATGGGA 541
QY 547 TGTGTTTTCCAGAGCACAGAGTGAACACGTGACCAAGTAGAATGATTTTCAGGA 606
Db 542 TGTGTTTTCCAGAGCACAGAGTGAACACGTGACCAAGTAGAATGATTTTCAGGA 601
QY 607 CGCGCGCAAGG 619
Db 602 CGCGCGCAAGG 614

RESULT 7

US-09-663-600A-50
; Sequence 50, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.053.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116

;; PRIOR FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: 60/099,273
;; PRIOR FILING DATE: 1998-09-04
;; NUMBER OF SEQ ID NOS: 229
;; SOFTWARE: Patent.pm
;; SEQ ID NO 50
;; LENGTH: 1158
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig_peptide
;; LOCATION: 214..339
;; OTHER INFORMATION: Von Heijne matrix
;; OTHER INFORMATION: score 6.09999990463257
;; OTHER INFORMATION: seq AILLQSQAYWA/LP
;; NAME/KEY: polyA signal
;; LOCATION: 1133..1138
;; NAME/KEY: polyA site
;; LOCATION: 1146..1158
;; NAME/KEY: misc_feature
;; LOCATION: 840..968
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id :H64717
;; OTHER INFORMATION: est
;; NAME/KEY: misc_feature
;; LOCATION: 858..968
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id :H65208
;; OTHER INFORMATION: est
;; NAME/KEY: misc_feature
;; LOCATION: 652
;; OTHER INFORMATION: n=a, g, c or t
US-09-663-600A-50

Query Match 29.8%; Score 485.6; DB 4; Length 1158;
Best Local Similarity 98.8%; Pred. No. 9.4e-153;
Matches 496; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 7 GAGTGCAGCTGGGGAGATTTCAGTGCATTCGCTCCCTCCCTGGTCTCTTCATCTTGGAT 66
Db 15 GACTGCAGCTGGGGAGATTTCAGTGCATTCGCTCCCTCCCTGGTCTCTTCATCTTGGAT 74

QY 67 TTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTGTTACTG 126
Db 75 TTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTGTTACTG 133

QY 127 GATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATGTG 186
Db 134 GATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATGTG 193

QY 187 GGTGATTCAGCTCTGATGGGATGTTTCCAGAGCAGAGACAAATGTATATTCAAG 246
Db 194 GGTGATTCAGCTCTGATGGGATGTTTCCAGAGCAGAGACAAATGTATATTCAAG 253

QY 247 ATAGACTGGACTCTGTCCACAGGAGAGCAGCCCAAGGACGAATATGTCTATATTAC 306
Db 254 ATAGACTGGACTCTGTCCACAGGAGAGCAGCCCAAGGACGAATATGTCTATATTAC 313

QY 307 TCCAACTCAGTGTGCTTATTTGGCGCTTCCAGAACCGCGTACACTTGATGGGGACATC 366
Db 314 TCCAACTCAGTGTGCTTATTTGGCGCTTCCAGAACCGCGTACACTTGATGGGGACATC 373

QY 367 TTATGCAATGATGCTCTCTCTCTCTCTCAAGATGTCAAGAGGCTGACCAGGACCTAT 426
Db 374 TTATGCAATGATGCTCTCTCTCTCTCAAGATGTCAAGAGGCTGACCAGGACCTAT 433

QY 427 ATCTGTGAAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAGCGGCTGATCTGCAT 486
Db 434 ATCTGTGAAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAGCGGCTGATCTGCAT 493

QY 487 GTGCTTCCAGAGGAGCCCAAG 508
Db 494 GTGCTTCCAGAGGAGCCCAAG 515

RESULT 8
US-09-663-600A-144
; Sequence 144, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 144
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 1133..1138
; NAME/KEY: polyA site
; LOCATION: 1146..1158
; NAME/KEY: misc_feature
; LOCATION: 652
; OTHER INFORMATION: n=a, g, c or t
US-09-663-600A-144

Query Match 29.8%; Score 485.6; DB 4; Length 1158;
Best Local Similarity 98.8%; Pred. No. 9.4e-153;
Matches 496; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 7 GAGTGCAGCTGGGGAGATTTCAGTGCATTCGCTCCCTCCCTGGTCTCTTCATCTTGGAT 66
Db 15 GACTGCAGCTGGGGAGATTTCAGTGCATTCGCTCCCTCCCTGGTCTCTTCATCTTGGAT 74

QY 67 TTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTGTTACTG 126
Db 75 TTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTGTTACTG 133

QY 127 GATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATGTG 186
Db 134 GATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATGTG 193

QY 187 GGTGATTCAGCTCTGATGGGATGTTTCCAGAGCAGAGACAAATGTATATTCAAG 246
Db 194 GGTGATTCAGCTCTGATGGGATGTTTCCAGAGCAGAGACAAATGTATATTCAAG 253

QY 247 ATAGACTGGACTCTGTCCACAGGAGAGCAGCCCAAGGACGAATATGTCTATATTAC 306
Db 254 ATAGACTGGACTCTGTCCACAGGAGAGCAGCCCAAGGACGAATATGTCTATATTAC 313

QY 307 TCCAACTCAGTGTGCTTATTTGGCGCTTCCAGAACCGCGTACACTTGATGGGGACATC 366
Db 314 TCCAACTCAGTGTGCTTATTTGGCGCTTCCAGAACCGCGTACACTTGATGGGGACATC 373

QY 367 TTATGCAATGATGCTCTCTCTCTCTCTCAAGATGTCAAGAGGCTGACCAGGACCTAT 426


```
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1549
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-1549

Query Match      2.5%; Score 40.6; DB 4; Length 438;
Best Local Similarity 52.0%; Pred. No. 0.0035;
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 730 GACGGTTCATCATCTTCAAGGAGTGGGGAGTCAGATGGAGGAACTACACCTGCAGT 789
Db 142 GACITTTACCTTCGACTAGAGGATGTGAGCCAGGCCAGGCTGGACCTACACCTGCCAT 201
QY 790 ATCCACCTAGGAACTCGTGTTCAGAAACCAATGTGCTGCATGTGAGCCCGGAAGAG 849
Db 202 ATCCATCTGCAGAACAGCAGCTCAATGCCATGTGCATGTGCAATCATCACAGTGACT 261
QY 850 CCTCGAAGCACTGGTACCCCGCAGCCCTGAGGCTCTGGTCTGGGTGGTAATC 904
Db 262 CCCAAATCCTTTGGGTACCTGGATCCCTGGGGAAGCTCTTTGTGAGGTGACTC 316

RESULT 12
US-09-614-124B-1549
; Sequence 1549, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1549
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-1549

Query Match      2.5%; Score 40.6; DB 4; Length 438;
Best Local Similarity 52.0%; Pred. No. 0.0035;
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 730 GACGGTTCATCATCTTCAAGGAGTGGGGAGTCAGATGGAGGAACTACACCTGCAGT 789
Db 142 GACITTTACCTTCGACTAGAGGATGTGAGCCAGGCCAGGCTGGACCTACACCTGCCAT 201
QY 790 ATCCACCTAGGAACTCGTGTTCAGAAACCAATGTGCTGCATGTGAGCCCGGAAGAG 849
Db 202 ATCCATCTGCAGAACAGCAGCTCAATGCCATGTGCATGTGCAATCATCACAGTGACT 261
QY 850 CCTCGAAGCACTGGTACCCCGCAGCCCTGAGGCTCTGGTCTGGGTGGTAATC 904
Db 262 CCCAAATCCTTTGGGTACCTGGATCCCTGGGGAAGCTCTTTGTGAGGTGACTC 316

RESULT 13
US-09-671-325-1549
; Sequence 1549, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1549
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-1549

Query Match      2.5%; Score 40.6; DB 4; Length 438;
Best Local Similarity 52.0%; Pred. No. 0.0035;
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 730 GACGGTTCATCATCTTCAAGGAGTGGGGAGTCAGATGGAGGAACTACACCTGCAGT 789
Db 142 GACITTTACCTTCGACTAGAGGATGTGAGCCAGGCCAGGCTGGACCTACACCTGCCAT 201
QY 790 ATCCACCTAGGAACTCGTGTTCAGAAACCAATGTGCTGCATGTGAGCCCGGAAGAG 849
Db 202 ATCCATCTGCAGAACAGCAGCTCAATGCCATGTGCATGTGCAATCATCACAGTGACT 261
QY 850 CCTCGAAGCACTGGTACCCCGCAGCCCTGAGGCTCTGGTCTGGGTGGTAATC 904
Db 262 CCCAAATCCTTTGGGTACCTGGATCCCTGGGGAAGCTCTTTGTGAGGTGACTC 316

RESULT 14
US-08-416-478A-1
; Sequence 1, Application US/08416478A
; Patent No. 5773578
; GENERAL INFORMATION:
; APPLICANT: Hercend, Thierry
; APPLICANT: Triebel, Frederic
; TITLE OF INVENTION: New Proteins Produced By Human
; TITLE OF INVENTION: Lymphocytes, DNA Sequences Encoding These Proteins And
; TITLE OF INVENTION: Their Pharmaceutical And Biological Uses
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416,478A
; FILING DATE: 04-APR-1995
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```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,644
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: HERCEND=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 231..1724
US-08-416-478A-1

Query Match 2.5%; Score 40.6; DB 1; Length 1871;
Best Local Similarity 52.0%; Pred.No. 0.01;
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 730 GACGGTTCCATCATGCTTCAAGAGTGAGGAGTGCAGATGGAGGAACTACACCTGCAGT 789
Db 1173 GACTTTACCCCTTCGACTAGAGGATGTGAGCCAGGCCCGAGCTGGGACCTACACCTGCCAT 1232

QY 790 ATCCACCTAGGAACTGGTGTTCAGAAACCATTGTCTGCATCTCAGCCCGGAAGAG 849
Db 1233 ATCCATCTCGAGGAACAGAGCTCAATGACATGTCACATTTGGCAATCATCAGTGACT 1292

QY 850 CCTCGAACACTGGTGACCCCGCAGCCCTGAGGCCTCTGCTCTTGGGTGTAATC 904
Db 1293 CCCAAATCCTTTGGGTCACTGGATCCCTGGGGAAGCTGCTTTGTGAGGTGACTC 1347

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RESULT 15
US-08-474-988B-1
; Sequence 1, Application US/08474988B
; Patent No. 5874250
; GENERAL INFORMATION:
; APPLICANT: Hercend, Thierry
; APPLICANT: Triebel, Frederic
; TITLE OF INVENTION: NEW PROTEINS PRODUCED BY HUMAN
; TITLE OF INVENTION: LYMPHOCYTES, DNA SEQUENCES ENCODING THESE PROTEINS AND
; TITLE OF INVENTION: THEIR PHARMACEUTICAL AND BIOLOGICAL USES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/474,988B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,478
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,644
; FILING DATE: 08-SEP-1992

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: HERCEND=1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1871 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 231..1724
US-08-474-988B-1

Query Match 2.5%; Score 40.6; DB 2; Length 1871;
Best Local Similarity 52.0%; Pred.No. 0.01;
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 730 GACGGTTCCATCATGCTTCAAGAGTGAGGAGTGCAGATGGAGGAACTACACCTGCAGT 789
Db 1173 GACTTTACCCCTTCGACTAGAGGATGTGAGCCAGGCCCGAGCTGGGACCTACACCTGCCAT 1232

QY 790 ATCCACCTAGGAACTGGTGTTCAGAAACCATTGTCTGCATCTCAGCCCGGAAGAG 849
Db 1233 ATCCATCTCGAGGAACAGAGCTCAATGACATGTCACATTTGGCAATCATCAGTGACT 1292

QY 850 CCTCGAACACTGGTGACCCCGCAGCCCTGAGGCCTCTGCTCTTGGGTGTAATC 904
Db 1293 CCCAAATCCTTTGGGTCACTGGATCCCTGGGGAAGCTGCTTTGTGAGGTGACTC 1347

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Job time : 147 secs

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OM nucleic - nucleic search, using sw model

Run on: October 1, 2004, 19:38:55 ; Search time 10107 Seconds
(without alignments)
6990.120 Million cell updates/sec

Title: US-09-989-728-421
Perfect score: 1630
Sequence: 1 cggctcgagtcgagctgtgg.....taaaaacccaacccaatcaa 1630

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5	1630	100.0	1630	6	AX454648	AX454648 Sequence
6	1630	100.0	1630	6	AX464386	AX464386 Sequence
7	1630	100.0	1630	6	AX491126	AX491126 Sequence
8	1630	100.0	1630	9	AY358362	AY358362 Homo sapi
9	1621.4	99.5	1751	6	BD248693	BD248693 Inflamm
10	1621.4	99.5	1751	6	AR373044	AR373044 Sequence
11	1621	99.4	1635	9	AY138965	AY138965 Homo sapi
12	1534.8	94.2	1561	6	AR225785	AR225785 Sequence
13	1534.8	94.2	1561	6	AX347902	AX347902 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AR252655 Sequence 421 from patent US 6478825. linear PAT 20-DEC-2002
DEFINITION AR252655
ACCESSION AR252655
VERSION AR252655.1 GI:27300563
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1630)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the treatment of bone defects
JOURNAL Patent: US 6478825-A 421 12-NOV-2002;

d. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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DB	1	CGGCTCGAGTCAGCTGTGGGAGATTTCAGTGCATTCGCTCCCTCGGTCCTTTCATC	60		
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DB	61	TTGGATTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTG	120		
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DB	121	TTACTGGATTATTCCTTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC	180		
QY	181	CATGTGGTGATTTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAACAATGTATA	240		
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QY	361	GACATCTTATGCAATGATGGCTCTCTCTGCTCCAGATGTGCAAGAGGCTGACACAGGA	420		
DB	361	GACATCTTATGCAATGATGGCTCTCTCTGCTCCAGATGTGCAAGAGGCTGACACAGGA	420		
QY	421	ACCTATATCTGTGAAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAGCGCGTGGTA	480		
DB	421	ACCTATATCTGTGAAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAGCGCGTGGTA	480		
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QY	841	CCGGAAGAGCCTCGAACACTGGTGACCCCGGACGCCCTGAGGCCCTTGGTCTTGGGTGGT	900		
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DB	901	AATCAGTTGGTGATCATTTGTGGGAATTTGTCTGTGCCCAAAATCTGCTGCTCCCTGTTCTG	960		

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Db	1021	AAGAACACGAAGAAGACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGT	1080
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Qy	1441	AGCTCTGGAGAAACAGGCTCTGAGGGGAGGGAGCATGGACTTGGCTCTGGAGTGGG	1500
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Db	1621	CCCAAAATCAA 1630	
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LOCUS		Sequence 195 from Patent WO0193983.	
DEFINITION		AX358942	
ACCESSION		AX358942	
VERSION		AX358942.1 GI:18675372	
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1	
AUTHORS		Baker, K.P., Desnovers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.	
TITLE		Secreted and transmembrane polypeptides and nucleic acids encoding the same	
JOURNAL		Patent: WO 0193983-A 195 13-DEC-2001; Genentech Inc. (US)	
FEATURES		Location/Qualifiers	
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ORIGIN	/db_xref="taxon:9606"		
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Db	121	TTACTGGATTATTCCTTGGGCTGAAATGACTTGAATGTTTCCCGCTGAGCTAACAGTC	180
QY	181	CATGTGGTGATTCAGCTCTGATGGATGTGTTTCCAGAGCACAGACAAATGTATA	240
Db	181	CATGTGGTGATTCAGCTCTGATGGATGTGTTTCCAGAGCACAGACAAATGTATA	240
QY	241	TTCCAGATAGACTGACTCTGTCAACAGAGAGCAGCCAAAGCAATATGTCTATAC	300
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QY	301	TATTAATCCAACTCAGTGTGCTTATTTGGGCGCTTCCAGAACCGGTACATTGATGGG	360
Db	301	TATTAATCCAACTCAGTGTGCTTATTTGGGCGCTTCCAGAACCGGTACATTGATGGG	360
QY	361	GACATCTTATGAAATGATGGCTCTCTCTGCTCCAAAGATGTCAAGAGGCTGACCAAGGA	420
Db	361	GACATCTTATGAAATGATGGCTCTCTCTGCTCCAAAGATGTCAAGAGGCTGACCAAGGA	420
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LOCUS	Sequence 195 from Patent WO0208288.		
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ACCESSION	AX362435.1	GI:18694675	
VERSION			
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Baker, K.P., Desnovers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., and Wood, W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0208288-A 195 31-JAN-2002; Genentech, Inc. (US)		
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ORIGIN			

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RESULT 4

AX403534

LOCUS

DEFINITION

AX403534

ACCESSION

VERSION

AX403534.1

GI:21437009

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

Ashkenazi, A. J., Baker, K. P., Botstein, D., Desnovers, L., Eaton, D.,

Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,

Grimaldi, C. J., Gurney, A. L., Kljavin, I., Napier, M. A., Pan, J.,

Paoni, N. F., Roy, M., Stewart, T. A., Tumas, D., Watanabe, C. K.,

Williams, P., Wood, W. I. and Zhang, Z.

Secreted and transmembrane polypeptides and nucleic acids encoding

the same

JOURNAL

Patent: WO 0073454-A 421 07-DEC-2000;

Genentech, Inc. (US)

Location/Qualifiers

1. .1630

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

FEATURES

source

ORIGIN

Query Match 100.0%; Score 1630; DB 6; Length 1630;

Best Local Similarity 100.0%; Pred. No. 0; Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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ACCESSION	AX454648		
VERSION	AX454648.1	GI:21713948	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.		
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis		
JOURNAL	Patent: WO 0208284-A 233 31-JAN-2002; Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)		
FEATURES	Location/Qualifiers		
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	/mol_type="unassigned DNA"		

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ORIGIN

Query Match 100.0%; Score 1630; DB 6; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 TTACTGGATTAATTCCTTGGGCTCGAATGACTTTGAATGTTTCCCGCTGAGCTAACAGTC 180
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QY 181 CATGTGGGTGATTCAGCTCTGATGGATGTGTTTCCAGAGCACAGAGCAAAATGTATA 240
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AX464386
LOCUS AX464386 1630 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 519 from Patent WO0140466.
ACCESSION AX464386
VERSION AX464386.1 GI:21899209
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tamas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 519 07-JUN-2001;
Genentech Inc. (US)
FEATURES
Location/Qualifiers
source 1..1630
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ORIGIN

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REFERENCE			
AUTHORS			
Baker, K.P., Ferrara, N., Gerber, H., Gertsen, M.E., Goddard, A.,			
Godowski, P.J., Gurney, A.B., Hillan, K.J., Marsters, S.A., Pan, J.,			
Faoni, N.F., Stephan, J.P., Watanabe, K.K., Williams, P.M., Wood, W.I.			
and Ye, W.			
TITLE			
Compositions and methods for the diagnosis and treatment of			
disorders involving angiogenesis			
JOURNAL			
Patent: WO 020690-A 233 03-JAN-2002;			
Genentech, Inc. (US)			
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Query Match 100.0%; Score 1630; DB 6; Length 1630;

Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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Db 121 TTACTGGATTATTCCTGGGCTCAATGACCTGATGTTTCCAGACACAGAAAGACAAATGATA 240

Qy 181 CATGGTGGTATTCAGTCTCTGATGGGATGTTTTCAGAGACACAGAAAGACAAATGATA 240
Db 181 CATGGTGGTATTCAGTCTCTGATGGGATGTTTTCAGAGACACAGAAAGACAAATGATA 240

Qy 241 TTCAAGATAGACTGACTCTGTACAGGAGACGACGCAAGGACGAAATATGCTATAC 300
Db 241 TTCAAGATAGACTGACTCTGTACAGGAGACGACGCAAGGACGAAATATGCTATAC 300

Qy 301 TATTACTCCAACTCAGTGTGCTTATGGGCGCTTCCAGACCCGCTACACTTGTATGGG 360
Db 301 TATTACTCCAACTCAGTGTGCTTATGGGCGCTTCCAGACCCGCTACACTTGTATGGG 360

Qy 361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAAGATGCAAGAGGCTGACACAGGA 420
Db 361 GACATCTTATGCAATGATGGCTCTCTCTGCTCCAAAGATGCAAGAGGCTGACACAGGA 420

Qy 421 ACCTATATCTGTAATTCGCTCAAGGGAGACGACGAGTGTTCAGAGCGCGTGGTA 480
Db 421 ACCTATATCTGTAATTCGCTCAAGGGAGACGACGAGTGTTCAGAGCGCGTGGTA 480

Qy 481 CTGCATGTGCTTCCAGAGGACCAAGAGCTCATGTCCTCATGTCGATGATGATGATTT 600
Db 481 CTGCATGTGCTTCCAGAGGACCAAGAGCTCATGTCCTCATGTCGATGATGATGATTT 600

Qy 541 ATGGGATGTGTTTTCAGAGACAGAAAGTGAACACAGTGAACCAAGGTAGATGATTT 600
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Qy 601 TCAGGACGGCGCGCAAGAGGAGATGATTTCTGTTACTACCAACAACTCAGGATGCT 660
Db 601 TCAGGACGGCGCGCAAGAGGAGATGATTTCTGTTACTACCAACAACTCAGGATGCT 660

Qy 661 GTGAGTACTCCAGAGCTGGGGCCACTTCAGAAATCGTGAACCTGTTGGGGGACATT 720
Db 661 GTGAGTACTCCAGAGCTGGGGCCACTTCAGAAATCGTGAACCTGTTGGGGGACATT 720

Qy 721 TTCGCAATGACGGTTCATCATGCTTCAAGAGTGAGGGAGTCAGATGGAGAACTAC 780
Db 721 TTCGCAATGACGGTTCATCATGCTTCAAGAGTGAGGGAGTCAGATGGAGAACTAC 780

Qy 781 ACCTGCAGTATCCACTAGGAAACCTGCTGTTCAGAAAAACCATTTGCTGTCATCTCAGC 840
Db 781 ACCTGCAGTATCCACTAGGAAACCTGCTGTTCAGAAAAACCATTTGCTGTCATCTCAGC 840

Qy 841 CCGAAGAGCCTCGAAACACTGCTGTCACCCCGCAGCCCTGAGGCTCTGCTTGGTGGT 900
Db 841 CCGAAGAGCCTCGAAACACTGCTGTCACCCCGCAGCCCTGAGGCTCTGCTTGGTGGT 900

Qy 901 AATCAGTTGGTGATCATTTGCTGGGAATTCCTGTCGCAAACTCCTGCTCCTCTTCTG 960
Db 901 AATCAGTTGGTGATCATTTGCTGGGAATTCCTGTCGCAAACTCCTGCTCCTCTTCTG 960

Qy 961 ATATTGATCGTGAAGAGACCTGTGGAATTAAGAGTTTCAAGTGAATTTTACAGTCTTGGT 1020
Db 961 ATATTGATCGTGAAGAGACCTGTGGAATTAAGAGTTTCAAGTGAATTTTACAGTCTTGGT 1020

Qy 1021 AAGAACAGAAAGAGACTAATCCAGAGATAAAGAAAAACCTGCTCCATTTTGAAGATGT 1080
Db 1021 AAGAACAGAAAGAGACTAATCCAGAGATAAAGAAAAACCTGCTCCATTTTGAAGATGT 1080

Qy 1081 GAAGGGAGAAACACTTTACTCCCAATATTTCTAGGGAGGTGATCGAGGAAGAGAA 1140
Db 1081 GAAGGGAGAAACACTTTACTCCCAATATTTCTAGGGAGGTGATCGAGGAAGAGAA 1140

Qy 1141 CCAAGTGAATAATCAGAGGCCACTTACATGACCATGCAACCCAGTTTGGCCCTTCTCTGAGG 1200
Db 1141 CCAAGTGAATAATCAGAGGCCACTTACATGACCATGCAACCCAGTTTGGCCCTTCTCTGAGG 1200

Qy 1201 TCAGATCGGAACACTCATTGAAAAAAGTCAGGTGGGGAATGCCAAAAACACAGCAA 1260
Db 1201 TCAGATCGGAACACTCATTGAAAAAAGTCAGGTGGGGAATGCCAAAAACACAGCAA 1260

Qy 1261 GCCTTTTGAGAAGAAATGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTCTGTG 1320
Db 1261 GCCTTTTGAGAAGAAATGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTCTGTG 1320

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Db 1321 TGTCTCTGGGCCACTCTACAGTGAATTCAGATCCCGCTCTCCAGCTGCTCTCTCTGT 1380

Qy 1381 CTCATTTGTTGTTCAATACACTGAAGATGGAGAAATTTGAGGCTTGGAGAGAGACTGAC 1440
Db 1381 CTCATTTGTTGTTCAATACACTGAAGATGGAGAAATTTGAGGCTTGGAGAGAGACTGAC 1440

Qy 1441 AGCTCTGGAGAAACAGGCTGCTGAGGGAGGGAGCATGAGCTTGGCTCTGGAGTGGG 1500
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Qy 1501 ACATGSCCTTGGGAACAGGCTGAGTGAATGGCTTCAAAACCCCGCTTGGATCAGACC 1560
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Qy 1561 CTCTGTGGCAGGGTCTTGTAGTGATGATTTACTGGGAAGAAATCAGAGATAAAACCAA 1620
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Qy 1621 CCCAAATCAA 1630
Db 1621 CCCAAATCAA 1630

RESULT 9

BD248693

LOCUS

BD248693

1751 bp

DNA

linear

PAT 17-JUL-2003


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Db      1668 TGGGCGAGGTTCTTAGTGATGAGTTACTTGGGAAGAAATCAGAGATAAAACCCAAA 1727
QY      1627 TCA 1629
Db      1728 TCA 1730

RESULT 10
AR373044 AR373044 1751 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 11 from patent US 6602667.
ACCESSION AR373044
VERSION AR373044.1 GI:40074969
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1751)
TITLES Walker, M.G., Volkmut, W. and Klingler, T.M.
JOURNAL Inflammation-associated polynucleotides
FEATURES Patent: US 6602667-A 11 05-AUG-2003;
Location/Qualifiers
source 1..1751
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ORIGIN

Query Match 99.5%; Score 1621.4; DB 6; Length 1751;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1622; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCTCCCTGGGTGCTCTTCACTTGGAT 66
Db      108 GACTGCAGCTGTGGGAGATTTCAGTGCATTGCCTCCCTGGGTGCTCTTCACTTGGAT 167

QY      67 TTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTGTACTG 126
Db      168 TTGAAAGTTGAGAGCAGCATGTTTGGCCACTGAAACTCATCTGCTGCCAGTGTACTG 227

QY      127 GATTATTCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATGTG 186
Db      228 GATTATTCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATGTG 287

QY      187 GGTGATTTCAGTCTGATGGGATGTTTCCAGAGCAGAGACAAATGATATTCAG 246
Db      288 GGTGATTTCAGTCTGATGGGATGTTTCCAGAGCAGAGACAAATGATATTCAG 347

QY      247 ATAGACTGGACTCTGTCCACAGGAGAGCAGCCAGGACGAATATGTGCTATATTAC 306
Db      348 ATAGACTGGACTCTGTCCACAGGAGAGCAGCCAGGACGAATATGTGCTATATTAC 407

QY      307 TCCAACTCAGTGTGCTATTGGGGGCTTCCAGAACCGGTACACTTGTATGGGGACATC 366
Db      408 TCCAACTCAGTGTGCTATTGGGGGCTTCCAGAACCGGTACACTTGTATGGGGACATC 467

QY      367 TTATGCAATGATGCTCTCTCTCTCCACAGATGTCAGAGGCTGACCGGAACTAT 426
Db      468 TTATGCAATGATGCTCTCTCTCTCCACAGATGTCAGAGGCTGACCGGAACTAT 527

QY      427 ATCTGTGAAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAGGGGCTGTACTGCAT 486
Db      528 ATCTGTGAAATCCGCTCAAGGGGAGAGCCAGGTGTTCAAGAGGGGCTGTACTGCAT 587

QY      487 GTGCTTCCAGAGAGCCCAAGAGCTCATGTCCATGTGGGTGAATTCAGATGGGA 546
Db      588 GTGCTTCCAGAGAGCCCAAGAGCTCATGTCCATGTGGGTGAATTCAGATGGGA 647

QY      547 TGTCTTTTCCAGAGCAGAGAGTCAACAGCTGACCAAGGTAGAAATGGATATTTTCA 606
Db      648 TGTCTTTTCCAGAGCAGAGAGTCAACAGCTGACCAAGGTAGAAATGGATATTTTCA 707

QY      607 CGGCGCGAAAGGAGGAGATTGTTATTTTCGTTACTTACCACAACTCAGAGTCTGTGGAG 666
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Db      708 CGGCGCGAAAGGAGGAGATTGTTATTTTCGTTACTACCACAACTCAGGATGCTGTGGAG 767
QY      667 TACTCCCAAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGGACATTTTCCGC 726
Db      768 TACTCCCAAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGGTGGGGGACATTTTCCGC 827
QY      727 AATGACGGTTCCATCATCTCTTCAAGGAGTGGGGAGTCAGATGGAGGAAATTCACCTGC 786
Db      828 AATGACGGTTCCATCATCTTCAAGGAGTGGGGAGTCAGATGGAGGAAATTCACCTGC 887
QY      787 AGTATCCACCTAGGAACTCGTGTTCAGAAACCAATGCTGCATCTCAGCCCGAA 846
Db      888 AGTATCCACCTAGGAACTCGTGTTCAGAAACCAATGCTGCATCTCAGCCCGAA 947
QY      847 GAGCTCGAACACTGTGTGACCCCGGACGCTCGAGGCTCTGGTCTTGGGTGTAATCAG 906
Db      948 GAGCTCGAACACTGTGTGACCCCGGACGCTCGAGGCTCTGGTCTTGGGTGTAATCAG 1007
QY      907 TTGTTGATCATTTGGGAAATTTCTGTGCCAATTCCTGTGCTGCCCTGTTCTGATATG 966
Db      1008 TTGTTGATCATTTGGGAAATTTCTGTGCCAATTCCTGTGCTGCCCTGTTCTGATATG 1067
QY      967 ATCTGTGAAGAGACTGTGTGAAATAAGAGTTTCAGTGAATTCACAGTCTTGGTGAAGAC 1026
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Db      1128 ACGAAGAGACTAATCCAGAGATAAAAGAAACCCCTGCCATTTTGAAGAATGTGAAGG 1187
QY      1087 GAGAAACACATTTACTCTCCCAATTAATTTGTACGGAGGTGATCGAGGAGAAAGAACCAAGT 1146
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QY      1147 GAAAAATCAGAGGCACCTCATGACCATGACCCAGTTTGGCCCTTCTCTGAGTGCAGAT 1206
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QY      1267 TGAGAAATGGAGAGTCCCTTCACTCAGCAGCGGTGGAGACTCTCTCTGTGTGTGTC 1326
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QY      1327 CTGGGCCACTCTACCACTGATTTTCAGACTCCCGCTCTCCAGCTGTCTCTCTGTCTCAT 1386
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QY      1387 GTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGACAGTCT 1446
Db      1488 GTTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGACAGTCT 1547
QY      1447 GGAGGAACAGCCTGCTGAGGGGAGGGAGCATGGAATTTGGCCTCTGGAGTGGAGACTG 1506
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QY      1507 GCCCTGGGAACCCAGGCTGAGTGGGCTCAAAACCCCGCTTGGATCAGACCTCTG 1566
Db      1508 GCCCTGGGAACCCAGGCTGAGTGGGCTCAAAACCCCGCTTGGATCAGACCTCTG 1667
QY      1567 TGGGCGGGTCTTCTAGTGGATGATTTACTGGGAAGATTCAGAGATAAAACCAACCCAAA 1626
Db      1668 TGGGCGGGTCTTCTAGTGGATGATTTACTGGGAAGATTCAGAGATAAAACCAACCCAAA 1727
QY      1627 TCA 1629
Db      1728 TCA 1730
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RESULT 11

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AV138965
LOCUS      AV138965      1635 bp      mRNA      linear      PRI 15-JAN-2003
DEFINITION Homo sapiens adhesion molecule AMICA (AMICA) mRNA, complete cds.
ACCESSION  AV138965
VERSION    AV138965.1  GI:27762121
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1635)
AUTHORS   Foster, J.S. and Gurney, A.L.
TITLE     Direct Submission
JOURNAL   Submitted (02-AUG-2002) Molecular Biology, Genentech, 1 DNA Way,
            South San Francisco, CA 94080, USA
FEATURES   Location/Qualifiers
            1..1635
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ORIGIN
Query Match      99.4%; Score 1621; DB 9; Length 1635;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      10  TGCAGCTGTGGGAGATTTCAGTCATTGCTCCCTCCCTGGTGCTCTTCATCTTGGATTG 69
DB      1  TGCAGCTGTGGGAGATTTCAGTCATTGCTCCCTCCCTGGTGCTCTTCATCTTGGATTG 60
QY      70  AAGTTGAGAGACAGCATGTTTGGCCACTGAACCTCATCTCTGCGCAGTGTTACTGGAT 129
DB      61  AAGTTGAGAGACAGCATGTTTGGCCACTGAACCTCATCTCTGCGCAGTGTTACTGGAT 120
QY      130  TATTCCTTGGGCGCTGAATGACTTGAATGTTTCCCGCGCTGAGCTAACAGTCCATGTGGT 189
DB      121  TATTCCTTGGGCGCTGAATGACTTGAATGTTTCCCGCGCTGAGCTAACAGTCCATGTGGT 180
QY      190  GATTCAGCTCTGATGGGATGTGTTTCCAGAGCAGACAGACAAATGTATATTCAAGATA 249
DB      181  GATTCAGCTCTGATGGGATGTGTTTCCAGAGCAGACAGACAAATGTATATTCAAGATA 240
QY      250  GACTGGACTCTGTCTACAGGAGAGACAGCCGAAGAGCGAATATGTGCTATATCTATCTCC 309
DB      241  GACTGGACTCTGTCTACAGGAGAGACAGCCGAAGAGCGAATATGTGCTATATCTATCTCC 300
QY      310  AATCTCAGTGTGCTTATGGGCGCTTCCAGAACCGGTACACTTGTATGGGGACATCTTA 369
DB      301  AATCTCAGTGTGCTTATGGGCGCTTCCAGAACCGGTACACTTGTATGGGGACATCTTA 360
QY      370  TGCATATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGAACAGGGAACCTATATC 429
DB      361  TGCATATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGAACAGGGAACCTATATC 420
QY      430  TGTGAATCCGCTCAAGAGGAGACCGAGGTGTTCAAGAGCGGTGTTACTGTGATGTG 489
DB      421  TGTGAATCCGCTCAAGAGGAGACCGAGGTGTTCAAGAGCGGTGTTACTGTGATGTG 480
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QY      550  GTTTTCCAGAGCAGACAGAAAGTGAAACACGTCGACCAAGGTAGAAATGATATTTTCAGGACGG 609
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QY      670  TCCCAGAGCTGCGGCCACTTCCAGAATCGTGTGAACCTGTGGGGGACATTTTCGCAAT 729
DB      661  TCCCAGAGCTGCGGCCACTTCCAGAATCGTGTGAACCTGTGGGGGACATTTTCGCAAT 720
QY      730  GACGGTTCATCATGCTTCAAGGAGTGAGGAGTCAGATGGAGGAAATACACCTGCACT 789
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DB      841  CCTCGAACACTGGTGACCCCGGAGCCTGAGGCTCTGGTCTTGGGTGGTAAATCAGTTG 900
QY      910  GTGATCATTTGGGAAATGTCTGTGCCAATCTGTGCTGCTCCCTGTTCTGATATTGATC 969
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DB      1021  AAGAGACTAATCCAGAGATAAAGAAACCCCTGCCATTTTGAAGATGTGAAGGGAG 1080
QY      1090  AAACACATTTACTCCCCAATAATTGTACGGAGGTGATCGAGGAAGAGAACCAAGTGA 1149
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DB      1141  AAATCAGAGGCCACTACATGACCATGACCCAGTTTGCCTTCTCTGAGGTTCAGATCG 1200
QY      1210  AACCACTCACTTGAACAAAGTACAGTGGGGGAATGCCAAACACAGCAAGCCTTTGA 1269
DB      1201  AACCACTCACTTGAACAAAGTACAGTGGGGGAATGCCAAACACAGCAAGCCTTTGA 1260
QY      1270  GAAGAATGGAGATCCCTTTCATCTCAGAGCGGTGGAGACTCTCTCTGTGTGTCTCTG 1329
DB      1261  GAAGAATGGAGATCCCTTTCATCTCAGAGCGGTGGAGACTCTCTCTGTGTGTCTCTG 1320
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DB      1321  GGCCACTCTACAGTGAATTCAGACTCCCGCTCTCCAGCTGTCTCTCTGTCTCAATTGT 1380
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Jarai,G. and Yousefi,S.
TITLE Novel gene
JOURNAL Patent: WO 0187938-A 18 22-NOV-2001;
FEATURES Location/Qualifiers
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Best Local Similarity 99.5%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
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QY 104 TCATCCTGTCGACGGTGTACTGGAATTAATCTTGGGCTGAATGACTGGAATGTTTCC 163
DB 62 TCATCCTGTCGACGGTGTACTGGAATTAATCTTGGGCTGAATGACTGGAATGTTTCC 121
QY 164 CGCTGAGCTACAGTCCAGTGGGTGATTCAGCTCTGATGGATGTTTTCAGAGCA 223
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QY 224 CAGAAGACAAATGTATATTCAGATAGACTGGACTCTGCACGAGAGACGCGCAAG 283
DB 182 CAGAAGACAAATGTATATTCAGATAGACTGGACTCTGCACGAGAGACGCGCAAG 241
QY 284 ACGAATATGTGTACTACTATTAATCTCAATCTCAGTGTGCTATTTGGGCTTCCAGAAC 343
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DB 302 GGTACACTTGTGGGGACATCTATGCAATGATGGCTCTCTCGTCCAGATGTC 361
QY 404 AAGAGCTGACACAGGAACTTATCTGTGAATCCGCTCAAGGGGAGAGCCAGGTGT 463
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QY 464 TCAAGAGCGGTGGTGTCTGCAATGTCCTTCCAGAGAGCCCAAGAGCTCATGGTCCATG 523
DB 422 TCAGGAAGCGGTGGTGTCTGCAATGTCCTTCCAGAGAGCCCAAGAGCTCATGGTCCATG 481
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QY 704 ACTGTGTGGGGACATTTTCCGCAATGAGGTTCCATCATGCTTCAAGAGTGGAGGT 763
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QY 944 TGCTGCTCCCTGTTCTCTGATATTGATCGTGAAGAACCTGTGGAATTAAGAGTTTCAGTGA 1003
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DEFINITION
ACCESSION BD209975
VERSION BD209975.1 GI:33019745
KEYWORDS JP 2002513554-A/47.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1649)
AUTHORS Hillman,J.L., Bandman,O., Lal,P., Yue,H., Reddy,R., Tang,T.Y., Gerstein,E.H., Patterson,C., Baughn,M.R., Azimzai,Y. and Lu,D.A.M.
TITLE Human transcriptional regulator molecules
JOURNAL Patent: JP 2002513554-A 47 14-MAY-2002;
COMMENT INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002513554-A/47
PD 14-MAY-2002
PF 04-MAY-1999 JP 2000547113
PR 05-MAY-1998 US 60/084254, 07-AUG-1998 US 60/095827 PR
02-OCT-1998 US 60/102745


```
PI JENNIFER L HILLMAN, OLGA BANDMAN, PREETI LAL, HENRY YUE, ROOPA PI
REDDY,
PI TOM Y TANG, EDWARD H GERSTIN, CHANDRA PATTERSON, MARIAH R BAUGHN,
PI YALDA AZIMZAI, DYUNG AINA M LU
PC C12N15/09, A61K38/00, A61K45/00, A61P35/00, A61P37/02, A61P43/00,
PC C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/68, C12P21/ PC
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DB |||
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ACCESSION
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VERSION
AX833028.1 GI:39919163
KEYWORDS
Homo sapiens (human)
SOURCE
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ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
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Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
Masuho, Y.
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Run on: October 1, 2004, 21:33:56 ; Search time 6328 Seconds

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Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	827.4	50.8	915	13	BX414034	BX414034 BX414034
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VERSION	AY420493.1	GI:39776450			
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
REFERENCE	1 (bases 1 to 911)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 911)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				


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VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 911)
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6071.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DG006DB08QPl&cluster=6071.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
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the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 51.3%; Score 836.2; DB 13; Length 911;
Best Local Similarity 98.8%; Pred. No. 8.4e-212;
Matches 849; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

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QY 65 ATTTCGAAGTTGAGAGCAGCATGTTTGGCCACTGAACTCATCTGCTGCCAGGTAC 124
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      AY420492.1 GI:39776449
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      1 (bases 1 to 911)
      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
      Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
      Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
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      Inferring nonneutral evolution from human-chimp-mouse orthologous
      gene trios
      Science 302 (5652), 1960-1963 (2003)
      JOURNAL
      PUBMED 14671302

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DEFINITION	BX414034 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA clone CS0DG006YD16 3-PRIME, mRNA sequence.		
ACCESSION	BX414034		
KEYWORDS	EST.		
SOURCE	Human		
ORGANISM	Homo sapiens (human)		
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AUTHORS	Li, W.B., Gruber, C., Jesse, J., and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6071.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0BAK046AB11NM1&cluster=6071.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0BAK046AB11NM1.		
FEATURES	Location/Qualifiers		
source	1..915 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DG006YD16" /tissue_type="B CELLS (RAMOS CELL LINE)" /cell_line="RAMOS CELL LINE" /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)" /notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."		
ORIGIN			
Query Match	50.8%;	Score 827.4;	DB 13; Length 915;
Best Local Similarity	96.7%;	Pred. No. 1.9e-209;	
Matches	887; Conservative	0; Mismatches 26; Indels 4; Gaps 4;	
Qy	711	GGGGGACATTTTCGCAATGACGGTTCCATCAT-GCTTCAAGGAGTCAGGAGTCAGATG	769
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Qy	770	GAGGAACCTACCTCGAGTATCCACTGAGGAACCTGGTTTCAGAAAAACCATTTGTC	829
Db	854	GAGGAACCTACCTCGAGTATCCACTGAGG-ACCTGGTGGTCAAAAAACCAATGTTTC	796
Qy	830	TGCATGTCAGCCGGGAAGAGCCTCGAACACTGGTGTACCCCGGAGCCCTCAGGCTCTGG	889

Db 795 TGCAAGTCAGCCCGAAGAGAGCCTCGAACACACTGGTGGCCCGGACCGCCTAAAGGCTCTGG 736
Qy 890 TCTTGGGTGTAATCAGTTGGTGTGATCATGTGGGAATTTCTGTGCCCAATCTGCTGCG 949
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Qy 950 TCCCTGTTCTCATATTGATCGTGAAGAGAGCCTGTGGAATAAAGAGTTTCAGTGAATTCCTA 1009
Db 675 TCCCTGTTCTCATATTGATCGTGAAGAGAGCCTGTGGAATAAAGAGTTTCAGTGAATTCCTA 616
Qy 1010 CAGTCTTGGTGAAGAACACGAGAGACTAATCCAGAGATAAAGAAACCCCTGCCATT 1069
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Qy 1070 TTGAAGATGTGAAGGGAGAGAAACATATTACTTCCCAATTAATTTGACGGAGGTTGATCG 1129
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Qy 1130 AGGAAGAAGAACCAAGTCAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGC 1189
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Qy 1250 AAACACAGACGCTTTTGAAGAGATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGAC 1309
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Qy 1310 TCTCTCTGTTGTCCTCGGCCACTCTACAGGATTTACAGACTCCGCTCTCCACG 1369
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Qy 1370 TGTCTCTGTTCTCATTTGTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCTGGCAG 1429
Db 255 TGTCTCTGTTCTCATTTGTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCTGGCAG 196
Qy 1430 AGAGACTGGACAGCTCTGGAGAAACAGGCTCTGAGGGAGGGAGCATGCACTGGCC 1489
Db 195 AGAGACTGGACAGCTCTGGAGAAACAGGCTCTGAGGGAGGGAGCATGCACTGGCC 136
Qy 1490 TCTGAGTGGGACACTGGGCCCTGGGAAACAGGCTGAGTGGGCTCAAAACCCCGCT 1549
Db 135 TCTGAGTGGGACACTGGGCCCTGGGAAACAGGCTGAGTGGGCTCAAAACCCCGC- 77
Qy 1550 TGGATCAGACCTCTCTGTTGGGAGGGTCTTATGATGATGATTTCTGGGAAAGATCAGAG 1609
Db 76 TGGATCAGACCTCTCTGTTGGGAGGGTCTTATGATGATGATTTCT- GGAAGATCAGAG 18
Qy 1610 ATAAAACCAACCCAAA 1626
Db 17 ATAAAGGCCAACCCAAA 1

RESULT 7
BM921974
LOCUS
DEFINITION BM921974 1015 bp mRNA linear EST 12-MAR-2002
AGENCY AGENT 6706977 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753591
5', mRNA sequence.
BM921974
BM921974.1 GI:19372353
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1015)
NIH-MGC <http://mgi.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12789 row: j column: 24
High quality sequence stop: 699.
Location/Qualifiers
1. .1015
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/mol_type="mRNA"
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/clone="IMAGE:5753591"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 49.1%; Score 800.2; DB 12; Length 1015;
Best Local Similarity 99.3%; Pred. No. 3.6e-202;
Matches 835; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy 19 GGGGAGATTTCAGTGCATTGCTCCCTGGGTCCTTCATCTTGATTTGAAGTTGAG 78
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Qy 79 AGCAGCATGTTTGGCCACTGAACTCATCTGCTGCCAGTGTACTGGATTATTCCTTG 138
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Qy 139 GGCCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATGTGGTGATTCAGCT 198
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Db 209 CTGATGGGATGTTTCCAGAGCACAGAACAAATGTATTTCAAGATAGACTGGACT 268
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Qy 319 GTGCTTATTTGGCGCTTCCAGAACCGCTACACTTGTATGGGGAGACATCTTATGCAATGAT 378
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Qy 439 CGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAGGGCGGTGATCTGCATGTGTTCCAGAG 498
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Db 509 GAGCCCAAGAGACTCATGTCATCTGGTGCATTTGATTCAGTGGGATGTTTTCAGAG 568
Qy 559 AGCAGCAAGAGTGAACACACGTGACCAAGGTAGAAATGGAATTTTTCAGGACGGCGCAAG 618
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QY 619 GAGGAGATTGTAATTCGTTACTACCAAACTCAGGATGCTGTGGAGTACTCCAGAGC 678
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QY 739 ATCATGCTTCAAGGAGTGTGGAGTGTGAGTGTGAGGAACTACACCTGCGAGTATCCACCTA 798
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QY 799 -GGGAACCTGTGTGTTCAGAAAAACA-TTGTGCTGCATGTGAG-CCCGGAAGAGCTCGA 855
DB 809 GGGGAACCTGTGTGTTCAGAAAAACA-TTGTGCTGCATGTGAG-CCCGGAAGAGCTCGA 868
QY 856 A 856
DB 869 A 869

BI838890 849 bp mRNA linear EST 04-OCT-2001
603087272F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5226473 5',
mRNA sequence.
BI838890
BI838890.1 GI:15950440
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 849)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11569 Row: 0 Column: 18
High quality sequence start: 5
High quality sequence stop: 849.
Location/Qualifiers
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/mol_type="mRNA"
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/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dr primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

FEATURES
source
ORIGIN
Query Match 48.6%; Score 791.4; DB 12; Length 849;
Best Local Similarity 98.8%; Pred No. 7.4e-200;
Matches 839; Conservative 0; Mismatches 6; Indels 4; Gaps 4;
QY 673 CAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGTGGGGGACATTTTCCGCAATGAC 732

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DB 1 CAGAGCTGGGGCCACTTCCAGAAATCGTGTGAACCTGTGGGGGACATTTTCCGCAATGAC 60
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DB 121 CACCTAGGAACTGTGTTCAGAAAAACCATTTGTGCTGCATGTGAGCCCGGAAGAGCT 180
QY 853 CGAAACACTGTGTGACCCCGGAGCCCTGAGGCTCTGTGGGTGGTAACTCAGTTGGT 912
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QY 913 ATCATTTGGGAAATTTGCTGTGCCCAATCTGCTGTCTCCCTGTTCTGATATTGATCGTG 972
DB 241 ATCATTTGGGAAATTTGCTGTGCCCAATCTGCTGTCTCCCTGTTCTGATATTGATCGTG 300
QY 973 AAGAGACCTGTGGAATAAGAGTTTCACTGAATTTCTACAGTCTTGGTGAAGAACAGAG 1032
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QY 1033 AAGACTTAATCCAGAGATAAAAGAAAAACCTGCGCAATTTTGAAGATGTGAAGGGAGAA 1092
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DB 661 CACTCTACCAAGTATTTTCAAGTGTCCCGCTCTCTCCAGTGTCTCTCTCTCTCTCTCTCT 720
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QY 1450 GGAACAGGCTT-GCTGAGGGGAGGGAGCATGTGAGCTTTGGCTCTTGGAGTGGGACACTGGC 1508
DB 781 GGAACAGGCTTGGCTGAGGGGAGGGAGCATGTGAGCTTTGGCTCTTGGAGTGGGAGCTGGC 840
QY 1509 CCTGGGGAAC 1517
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RESULT 9
LOCUS BX346273/c
DEFINITION BX346273 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL002YK08 3-PRIME, mRNA sequence.
ACCESSION BX346273
VERSION BX346273.1 GI:30379079
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1079)

```

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 6071.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0AL002BF04NP1&cluster=6071.r. Contact :
 Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0AL002BF04NP1.
 Location/Qualifiers
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 /organism="Homo sapiens"
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
 source

ORIGIN
 Query Match 45.4%; Score 739.8; DB 13; Length 1079;
 Best Local Similarity 96.2%; Pred. No. 5e-186;
 Matches 781; Conservative 7; Mismatches 21; Indels 3; Gaps 3;

QY 818 AAACCATTTGCTGATGCTCAGCCGGAAGACCTCGAACATCTGGTACCCCGGAGGCC 877
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 DB 797 AACCTGGCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTTCCCAATAATTGTAC 738
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 DB 737 GGGAGGTGATCGAGAGAAACCAAGTGAATATCAGAGCCACCTACATGACCATGC 678
 QY 1178 ACCCAGTTTGGCTTCTCTGAGTCCAGATCGGAAACCACTCACTTGAATAAAGTCCAGGTG 1237
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 QY 1358 CGCTCTCCAGCTGTCTCTCTGTTCTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTT 1417

DB 497 CGCTCTCCAGCTGTCTCTCTGTTCTCATTGTTTGGTCAATACACTGAAGATGGAGAAATTT 438
 QY 1418 GGAGCTTGGCAGAGAGACTGGACAGCTCTGAGGAAACAGGCTCTCTGAGGCGAGGAGC 1477
 DB 437 GGAGCTTGGCAGAGAGACTGGACAGCTCTGAGGAAACAGGCTCTCTGAGGCGAGGAGC 378
 QY 1478 ATGACTTGGCTCTCTGAGTGGGACACTGGCCCTGGGAAACAGGCTGAGTGGGCT 1537
 DB 377 ATGACTTGGCTCTCTGAGTGGGACACTGGCCCTGGGAAACAGGCTGAGTGGGCT 318
 QY 1538 CAAACCCCTCTGGATCAGACCTCTCTGTTGGGAGGGTCTTCTAGTGGATGAGTACTGG 1597
 DB 317 CAAACCCCTCTGGATCAGACCTCTCTGTTGGGAGGGTCTTCTAGTGGATGAGTACTGG 258
 QY 1598 GAAGAATCAGAGATAAATAACCAACCAATCA 1629
 DB 257 GAAGAATCAGAGATAAATAACCAACCAATCA 226

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 ACCESSION BI767696
 VERSION BI767696.1 GI:15759274
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 790)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11526 row: h column: 13
 High quality sequence stop: 776.
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 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
 anonymous pool of 24 week female lung, 16 week female
 spleen, and 20-22 week male spleens. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 026. Note:
 this is a NIH_MGC Library."

ORIGIN
 Query Match 45.1%; Score 735; DB 12; Length 790;
 Best Local Similarity 98.9%; Pred. No. 8.3e-185;
 Matches 782; Conservative 0; Mismatches 5; Indels 4; Gaps 4;

QY 11 GCAGCTGTGGGAGATTTTCAGTGCATTCCTCCCTGGGTCTCTTCATCTTGATTTGA 70
 DB 1 GCAGCTGTGGGAGATTTTCAGTGCATTCCTCCCTGGGTCTCTTCATCTTGATTTGA 60

McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cf.html>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
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/clone_lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCCTAC.
TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"

ORIGIN

Query Match 42.4%; Score 691; DB 14; Length 710;
Best Local Similarity 95.6%; Pred. No. 4.4e-173;
Matches 691; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 937 ACAATCTGCTGCTCCCTGTTCTCATATTGATCGTGAAGAGACCTGTGGAAATAAGAGT 996
DB 710 ACAATCTGCTGCTCCCTGTTCTCATATTGATCGTGAAGAGACCTGTGGAAATAAGAGT 651
QY 997 TCAGTGAATTTACAGTCTTGGTGAAGAACACGGAAGAGACTAATCCAGAGATAAAGAA 1056
DB 650 TCAGTGAATTTACAGTCTTGGTGAAGAACACGGAAGAGACTAATCCAGAGATAAAGAA 591
QY 1057 AAACCTCGCCATTTTGAAGATGTGAAGGGAGAGAACACATTTTACTCCCAATAATTGTA 1116
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QY 1117 CGGAGGTGATCGAGGAAGAGAACCAAGTGAAGAAATCAGAGGCCACTTACATGACCATG 1176
DB 530 CGGAGGTGATCGAGGAAGAGAACCAAGTGAAGAAATCAGAGGCCACTTACATGACCATG 471
QY 1177 CACCCAGTTGGCCCTTCTGAGTGTCAGATCGGAACAACTCACTTGAAGAAAAGTCAGGT 1236
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DB 410 GGGGGAATGCCAAAACACAGACAGCTTTTGAGAAGAAATGGAGAGTCCCTTCATCTCAG 351

QY 1297 CAGCGGTGGAGACTCTCTCCTGTGTGTGTCTCTGGGCCACTCTTACCAGTGATTTCAGACTC 1356
DB 350 CAGCGGTGGAGACTCTCTCCTGTGTGTGTCTCTGGGCCACTCTTACCAGTGATTTCAGACTC 291
QY 1357 CGGCTCTCCAGCTGTCTCCTGTGTGTGTCTCTGGTCAATACACTGAGATGGAGAAAT 1416
DB 290 CGGCTCTCCAGCTGTCTCCTGTGTGTGTCTCTGGTCAATACACTGAGATGGAGAAAT 231
QY 1417 TGGAGCTTGGCAGAGAGACTGGACAGCTCTGGAGAACAGGCTCTCTGAGGGAGGGGAG 1476
DB 230 TGGAGCTTGGCAGAGAGACTGGACAGCTCTGGAGAACAGGCTCTCTGAGGGAGGGGAG 171
QY 1477 CATGCACTTGGCTCTGAGTGGGACACTGGCCCTGGGAACACGAGCTGAGTGAGTGGCC 1536
DB 170 CATGCACTTGGCTCTGAGTGGGACACTGGCCCTGGGAACACGAGCTGAGTGAGTGGCC 111
QY 1537 TCAAAACCCCGTGTGGATCAGACCCCTCTGTGGGAGGCTTCTTAGTGGATGAGTACTG 1596
DB 110 TCAAAACCCCGTGTGGATCAGACCCCTCTGTGGGAGGCTTCTTAGTGGATGAGTACTG 51
QY 1597 GGAAGATCAGAGATAAAACCAACCCAAATCAA 1630
DB 50 GGAAGATCAGAGATAAAACCAACCCAAATCAA 17

RESULT 14

BI818153 800 bp mRNA linear EST 04-OCT-2001
LOCUS 603032387P1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173820 5',
DEFINITION mRNA sequence.

ACCESSION

BI818153

VERSION

BI818153.1 GI:15928361

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L14M11432 row: m column: 21

High quality sequence start: 8

High quality sequence stop: 739.

Location/Qualifiers

1..800

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5173820"

/lab host="DH10B"

/clone lib="NIH_MGC_115"

/note="Organ: pooled brain, lung, testis; Vector:

pcmv-SpOFT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA

sample anonymous pool of 6 male brains, age range 23-27; 1

male lung, age 27; and 1 male testis, age 69. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.8 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

021. Note: this is a NIH_MGC Library."

ORIGIN

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Query Match 41.9%; Score 682.2; DB 12; Length 800;
Best Local Similarity 98.0%; Pred. No. 1e-170;
Matches 754; Conservative 0; Mismatches 8; Indels 7; Gaps 6;

QY 133 TCCTTGGGCGCTGAATGACTTGAATGTTTCCCGGCTGAGCTAACAGTCCATGTGGGTGAT 192
Db 9 TCCTTGGGCGCTGAATGACTTGAATGTTTCCCGGCTGAGCTAACAGTCCATGTGGGTGAT 67

QY 193 TCAGCTCTGATGGATGTTTTCAGAGCAGACAGAGCAAAATGATATTCAGATAGAC 252
Db 68 TCAGCTCTGATGGATGTTTTCAGAGCAGACAGAGCAAAATGATATTCAGATAGAC 127

QY 253 TGGACTCTGTCACAGGAGACAGCCCAAGAGCAATATGCTATATCTTACTTCCAAAT 312
Db 128 TGGACTCTGTCACAGGAGACAGCCCAAGAGCAATATGCTATATCTTACTTCCAAAT 187

QY 313 CTCAGTGTGCTATTTGGGCGCTTCAGAACCGCGTACACTTGTATGGGGGACATCTTATGC 372
Db 188 CTCAGTGTGCTATTTGGGCGCTTCAGAACCGCGTACACTTGTATGGGGGACATCTTATGC 247

QY 373 AATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 432
Db 248 AATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 306

QY 433 GAATCCGCTCAAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 492
Db 307 GAATCCGCTCAAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 366

QY 493 CCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 552
Db 367 CCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 426

QY 553 TTCCAGAGCAGAGAGTGAACACAGTGAACAGTGAACAGTGAACAGTGAACAGTGAACAGT 612
Db 427 TTCCAGAGCAGAGAGTGAACACAGTGAACAGTGAACAGTGAACAGTGAACAGTGAACAGT 486

QY 613 GCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 672
Db 487 GCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 546

QY 673 CAGAG-CTGGGCGCACTTCCAGAGTCTGTGTAACCTGTGGGGGACATTTTCCGCAATGA 731
Db 547 CAGAGACTGGGCGCACTTCCAGAGTCTGTGTAACCTGTGGGGGACATTTTCCGCAATGA 606

QY 732 CGGTTCATCATGCTTCAAGGAGTGAAGGA-CTCAGATGGAGGAACATACA-CTTGCAAT 789
Db 607 CGGTTCATCATGCTTCAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAG 666

QY 790 ATCCACCTAGGG- -AACCTGGTGTTCAGAGAAACCATTTGCTGATGTCAGCCCGGAAG 847
Db 667 ATCCACCTAGGGAAACCTTGTGTTTCAAGAAACCATTTGCTGATGTCAGCCCGGAAG 726

QY 848 AGCCTCGAACACTGTGTGACCCCGGCGACCCCTGAGGCGCTCTGTCTTTGGG 896
Db 727 AGCCTCGAACACTGTGTGACCCCGGCTGAGGCGCTCTGTCTTTGGG 775
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```
RESULT 15
CA748568/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
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CA748568 687 bp mRNA linear EST 26-NOV-2002
UI-H-Ftl-bhs-f-08-0-UI.s1 NCI CGAP Ftl Homo sapiens cDNA clone
UI-H-Ftl-bhs-f-08-0-UI 3', mRNA sequence.
CA748568
CA748568.1 GI:25568447
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 687)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: csap88-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bentso-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1. .687
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-Ftl-bhs-f-08-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ftl"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
NCI CGAP Ftl is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
normalized according to Ronaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an Ecor I adaptor,
digested with Not I, and cloned directionally into
pT73-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATCGCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Aveolar Macrophage
TAG LIB=UI-H-Ftl
TAG_SEQ=GGCCATCGCG"

ORIGIN

Query Match 40.7%; Score 663.6; DB 14; Length 687;
Best Local Similarity 99.3%; Pred. No. 9.1e-166;
Matches 666; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 960 GATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTTCAGTGAATTTACAGTCTTGGT 1019
Db 687 GATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTTCAGTGAATTTACAGTCTTGGT 628
QY 1020 GAAGAACACGAGAGAGACTTAATCCAGAGATAAAGAAAACCTGCCATTTTGAAGAATG 1079
Db 627 GAAGAACACGAGAGAGCTTAATCCAGAGATAAAGAAAACCTGCCATTTTGAAGAATG 568
QY 1080 TGAAGGGGAGAGAACACATTTTCTCCCAATAATTTACGGGAGGTGATCGAGAGAGAGA 1139
Db 567 TGAAGGGGAGAGAACACATTTTCTCCCAATAATTTACGGGAGGTGATCGAGAGAGAGA 508
QY 1140 ACCAGTGAATAATCAGAGGCCACCTATGACCATGACCCAGTTTGGCCTTCTCTGAG 1199
Db 507 ACCAGTGAATAATCAGAGGCCACCTATGACCATGACCCAGTTTGGCCTTCTCTGAG 448
QY 1200 GTCCAGTCGGAACAACTCCTTGAAGAAAAGTCAGTGGGGGAATGCCAAAACACAGCA 1259
Db 447 GTCCAGTCGGAACAACTCCTTGAAGAAAAGTCAGTGGGGGAATGCCAAAACACAGCA 388
QY 1260 AGCCTTTGAGAGAAATGGAGAGTCCCTTCATCTCAGAGCGGTGGAGACTCTCTCTGT 1319
Db 387 AGCCTTTGAGAGAAATGGAGAGTCCCTTCATCTCAGAGCGGTGGAGACTCTCTCTGT 328
QY 1320 GTGTGTCCTGGGCCACTCTTACCAGTGATTTTACAGTCCCGCTCTCCACACTGTCTCTCTG 1379
Db 327 GTGTGTCCTGGGCCACTCTTACCAGTGATTTTACAGTCCCGCTCTCCACACTGTCTCTCTG 268

Qy	1380	TCTCATTTGTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGA	1439
Db	267	TCTCATTTGTTGGTCAATACACTGAAGATGGAGAAATTTGGAGCCTGGCAGAGAGACTGGA	208
Qy	1440	CAGCTCTGGAGGAACAGGCCTGCTCAGGGGAGGAGCATGGACTTGGCCTCTGGAGTGG	1499
Db	207	CAGCTCTGGAGGAACAGGCCTGCTCAGGGGAGGAGCATGGACTTGGCCTCTGGAGTGG	148
Qy	1500	GACACTGGCCCTGGGAACGAGCTGAGCTGAGTGGCCTCAAACCCCGTTGGATCAGAC	1559
Db	147	GACACTGGCCCTGGGAACGAGCTGAGCTGAGTGGCCTCAAACCCCGTTGGATCAGAC	88
Qy	1560	CCTCCTGTGGGAGGCTTCTTAGTGGATGAGTTACTGGGAAGATCAGAGATAAAACCA	1619
Db	87	CCTCCTGTGGGAGGCTTCTTAGTGGATGAGTTACTGGGAAGATCAGAGATAAAACCA	28
Qy	1620	ACCCAAATCAA	1630
Db	27	ACCCAAATCAA	17

Search completed: October 2, 2004, 05:02:57
 Job time : 6335 secs

Blank

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 20:59:40 ; Search time 40 Seconds
(without alignments)
947.487 Million cell updates/sec

Title: US-09-989-728-422
Perfect score: 2067
Sequence: 1 MFCEPLKLLPVLDDYSLGL.....RNNSLKKSGGMPKTKQAF 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	183	8.9	365	2	JC7780	coxsackie- and ade
2	147	7.1	584	2	T08678	hypothetical prote
3	146.5	7.1	246	1	A22999	myelin P0 protein
4	140.5	6.8	249	1	A61087	myelin P0 glycopro
5	137	6.6	338	2	JC4776	limbic-system-asso
6	133	6.4	251	2	I38053	myelin protein zer
7	132.5	6.4	186	2	I61783	sodium channel bet
8	132	6.4	248	1	JH0252	myelin P0 protein
9	131	6.3	219	1	A29128	myelin P0 protein
10	130	6.3	248	1	MPRT0	myelin P0 protein
11	127.5	6.2	215	2	A57843	sodium channel bet
12	126	6.1	1028	2	A53449	plasmacytoma-assoc
13	125.5	6.1	509	2	JC5288	SHP substrate-1 pr
14	125.5	6.1	1040	2	A57638	receptor tyrosine
15	125.5	6.1	1103	2	T28899	hypothetical prote
16	125.5	6.1	1232	2	T43027	neural cell adhesi
17	123.5	6.0	285	2	S36903	Fc gamma (IgG) rec
18	123.5	6.0	1363	2	I58375	protein-tyrosine k
19	122.5	5.9	247	1	A54662	myelin P0 protein
20	122.5	5.9	338	2	JC5519	50K glycoprotein p
21	121.5	5.9	5175	2	T20992	hypothetical prote
22	121.5	5.9	5198	2	T43290	hemocentin precurs
23	120.5	5.8	1379	2	JC4954	vascular endotheli
24	119	5.8	321	2	I54766	B-lymphocyte activ
25	119	5.8	764	1	ORHUGS	secretory componen
26	118.5	5.7	317	2	JI0118	Fc gamma (IgG) rec
27	118.5	5.7	1298	2	A48999	protein-tyrosine k
28	118	5.7	333	2	A31923	analgain protein pr
29	118	5.7	898	2	A40114	fasciclin II precu

30	116.5	5.6	513	2	JC5289	SHP substrate-1 pr
31	116	5.6	1896	2	T08851	Down syndrome cell
32	115.5	5.6	271	2	A53268	T-cell receptor al
33	114	5.5	847	2	JH0371	B-cell adhesion pr
34	114	5.5	1028	2	I58164	BIG-1 protein - ra
35	111.5	5.4	4391	2	A38096	perlecan precursor
36	111.5	5.4	7962	2	I38346	elastic titin - hu
37	110.5	5.3	330	2	A29915	teratocarcinoma gl
38	109.5	5.3	1323	2	FN0568	connectin 3B - chi
39	109	5.3	1348	2	S51656	vascular endotheli
40	108.5	5.2	299	2	S56749	junctional adhesio
41	108.5	5.2	475	2	I76668	pregnancy-specific
42	108.5	5.2	662	2	T16525	hypothetical prote
43	108.5	5.2	3707	2	S18252	heparan sulfate pr
44	108	5.2	364	2	A30521	myeloid cell surfa
45	107.5	5.2	323	2	S06946	Fc gamma (IgG) rec

ALIGNMENTS

RESULT 1

JC7780

coxsackie- and adenovirus receptor - bovine
C:Species: Bos primigenius taurus (cattle)

C>Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002

C:Accession: JC7780

R:Thoeelen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.

Biochem. Biophys. Res. Commun. 288, 805-808, 2001

A>Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recepto

A:Reference number: JC7780

A:Contents: Liver

A:Accession: JC7780

A:Molecule type: mRNA

A:Residues: 1-365 <THO>

A:Cross-references: GB:AY033651

C:Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match 8.9%; Score 183; DB 2; Length 365;

Best Local Similarity 23.9%; Pred. No. 1.1e-06;

Matches 95; Conservative 61; Mismatches 146; Indels 96; Gaps 20;

QY	5	LKLILLPVLDDYSLGLNDLVNSPPELTVH--VGSALMGCVFO-STEDKCFKIDWTLSLP	61
Db	5	LRFLLLCGVADFTRG---LSITTEQMLEKAKGETAYLPCKFTLGPEDQGLDIEWLLSP	61
QY	62	GEHARDEVLYYYGNLSVPIGRFQ--RVHL-MGDILCNDGSLLDQVQADQTYICE	117
Db	62	ADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKSGDASINVTLNQLSDIGTYQCK	121
QY	118	IRLKGESQVFKAVLHLVLPPEPKELMVHVGGLIOMGCVFQSTEVKHVTKVFIISGRR	177
Db	122	V--KKAPGVGNKKIQLTVL-VKPSGIRCYVDGSEIGNDFK-----LKCE-----P	164
QY	178	KE-EIVERY-YHKLRMSEVSQSWGHQNRVNLVGDIFRNDGSLMVGRESGNGVTC	235
Db	165	KEGSLPIRYEWMKLSDSQKLPSTW-----LPMTSPV-----TSVNKASAEYSGT	213
QY	236	IHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVGNQLVIVIGIVCATILLPLVILI	295
Db	214	VR--NRVGSQCLLRLDVVP-----SNRAGTAGAVIGTLLAL-VLIAL	255
QY	296	VKKTGKGNSSVNTLVNKTNPKEIKPKCHPERCEGKHVSPVIVREVIEEPEPSE	355
Db	256	IVFCC-----HKRREKYEKEVHD-----IREDVPPP	284
QY	356	KSEATYTMHPVWPSLSDRNN--SLEKSGGGMPKTKQ	391
Db	285	KRSTSTARSY-----IGSNHSLGSMSPSNMEGYSKTKQ	317

RESULT 2

T08678

Db 40 VGSVDVTLVCGFMSNVEYSDLTTLTSLWRFRPDNKRDIISIFHYGN-----GVPIVKWGPGRG 95

Qy 205 RVNLVGDIFRNDGSIIMLQGVRESGNGNYTCSHLGNLVFKKTLVLHVSPPEPRLVTPAA 264
 Db 96 KVEWVGIDSKHDSIVIRNLDYDNGTFTCDVKNPPDVGTSSDVHLTVYD-----K 147

Qy 265 LRPLVGGNQLVVIIGVICATILLPLVLI-----IVKTKCGNKSS 305

Db 148 IPPVGAG-----VVSAGIIGTFLGIILLVGGLYFRYIVRRRARSSETS 191

RESULT 4

A61087

myelin P0 glycoprotein precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000

C:Accession: A61087

J. Neurosci. Res. 25, 143-151, 1990

A:Title: Molecular cloning of cDNAs that encode the chicken P0 protein: evidence for ear

A:Reference number: A61087; MUID:90204597; PMID:1690817

A:Accession: A61087

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-249 <BAR>

C:Comment: This protein is found only in peripheral nervous system Schwann cells.

C:Superfamily: myelin P0 protein; immunoglobulin homology

C:Keywords: glycoprotein; myelin; Schwann cell; structural protein; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-249/Product: myelin P0 glycoprotein #status predicted <WAT>

F:30-153/Domain: extracellular #status predicted <EXT>

F:43-129/Domain: immunoglobulin homology <IMM>

F:154-179/Domain: transmembrane #status predicted <TMW>

F:180-249/Domain: intracellular #status predicted <INT>

F:122/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 6.8%; Score 140.5; DB 1; Length 249;

Best Local Similarity 26.6%; Pred. NO. 0.0014;

Matches 45; Conservative 34; Mismatches 70; Indels 19; Gaps 7;

Qy 131 VVLHVPPEPKMLVHVHGLIOMGCVFQSTE-VKHVTKVEMIFSGRRRAKEIVFRYHKL 189
 Db 28 LAIHVY--TPREYGVGVSHVTLSCFSWSEWISEDISTYHWFQAEGRSDSISIFHYCK- 84

Qy 190 RMSVEYSOSGWHFQNRVNLVGDIFRNDGSIIMLQGVRESGNGNYTCSI-HLGNLVFKKT-I 247

Db 85 --GQPIYIDVGSFKERMVEWGRPRKDGSIIVHNLDTYDNGTFTCDVKNPPDIVGKSSQV 142

Qy 248 VLHVSPEEPRTLVTPAALRPLVGGNQLVVIIGVICATILLPLVLI 295

Db 143 TLVLEKUPTRY-----GVVLGS-----IIGGVLLLVALLVAVVYL 179

RESULT 5

JC4776

limbic-system-associated membrane protein precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 19-May-2000

C:Accession: JC4776

R.Pimenta, A.F.; Fischer, I.; Levitt, P.

Gene 170, 189-195, 1996

A:Title: cDNA cloning and structural analysis of the human limbic-system-associated memb

A:Reference number: JC4776; MUID:96235133; PMID:8666243

A:Accession: JC4776

A:Molecule type: mRNA

A:Residues: 1-338 <PIM>

A:Cross-references: GB:U41901; NID:g1276898; PIDN:AAC50569.1; PID:g1276899

A:Experimental source: brain

C:Comment: This is a neuronal surface glycoprotein distributed in cortical and subcortic

C:Genetics:

A:Gene: lamp

C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi

C:Keywords: brain; glycoprotein; membrane protein; phosphoprotein

F:1-7/Domain: signal sequence #status predicted <SIG>

F:333-338/Region: hydrophobic
F:40,66,136,148,279,300,315/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:42,115,142,164,171,220,231/Binding site: phosphate (Thr) (covalent) #status predicted
F:95,192,204,236,310/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 6.6%; Score 137; DB 2; Length 338;
Best Local Similarity 20.1%; Pred. No. 0.0039;
Matches 72; Conservative 54; Mismatches 123; Indels 110; Gaps 14;

Qy 4 PLKLLPLVLDYSLGN--DLNVSPPPLTVHVGDSALMGCVFQSTEDK-----CIF 53
Db 13 PLVLLRLCLPTGLPVRSDVFNRTDITVRQDGTALRCVLEDKSKVAWLNKRGIIIF 72
Qy 54 --KIDWTLSPEGEAKDEVLYYNSLNVPIGRFQNRVHLMGDILCDNGSLILQDVQADQ 111
Db 73 AGHKWLSLDRVLEKHSLEY-----SLRIQKVDVYDE 106
Qy 112 GTYICEIRLKGESQVFKKAVLVHLPE---EPKELMVHVGGLIQMGCVFQSTEV---K 163
Db 107 GSYTCVQTOHEPKTSQVYLIVQVPPKISNITSSDVTYNEGNSVTLVCWANGPEPVIWTR 166
Qy 164 HVTKEVIFSGR-----RAKEEIVFRYHKLKMSVEY-----SQS 198
Db 167 HLTPTRGEFEGBEYLEILGITREQSGKYECKAANEVSSADVQKVTVNYPPTITESKS 226
Qy 199 -----WGHFQNRVNLVG--DIFRNDG--SIMLQGVRESGG 230
Db 227 NEATGQASLKCSASAVPDPFWYRDDTRINSANGLEIKSTEGQSLSLTVNTYTEHYG 286
Qy 231 NYTCSIHGLNLFVFKKTVLHVSPEEPTLVTPAALPLVLGNGNLVIIVGIVCATILL 289
Db 287 NYTC-----VAANKLGVTNAS-----LVLPFGSVRG-INGSIASLVPLWLLASLLJCL 334

RESULT 6
I38053
myelin protein zero - human
C:Species: Homo sapiens (man)
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 21-Jan-2000
C:Accession: I38053; A49643; S43191
R:Rautenstrauss, B.; Nelis, E.; Grehl, H.; Pfeiffer, R.A.; Van Broeckhoven, C.
Hum. Mol. Genet. 3, 1701-1702, 1994
A:Title: Identification of a de novo insertional mutation in P0 in a patient with a Deje
A:Reference number: I38053; MUID:95135435; PMID:7530550
A:Accession: I38053
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-251 <RES>
A:Cross-references: EMBL:Z31718; NID:9469516; PIDN:CAAB3513.1; PID:9469517
R:Su, Y.; Brooks, D.G.; Li, L.; Lepercq, J.; Trofatter, J.A.; Ravetch, J.V.; Lebo, R.V.
Proc. Natl. Acad. Sci. U.S.A. 90, 10856-10860, 1993
A:Title: Myelin protein zero gene mutated in Charcot-Marie-Tooth type 1B patients.
A:Reference number: A49643; MUID:94068501; PMID:7504284
A:Accession: A49643
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 50-105 <SU1>
A:Experimental source: peripheral blood
A:Note: sequence extracted from NCBI backbone (NCBIP:139777)
C:Genetics:
A:Gene: GDB:MP2; CMT1B; CMT1
A:Cross-references: GDB:125266; OMIM:159440
A:Map position: lq22-lq23
C:Superfamily: myelin P0 protein; immunoglobulin homology
F:43-129/Domain: immunoglobulin homology <IMM>

Query Match 6.4%; Score 133; DB 2; Length 251;
Best Local Similarity 23.7%; Pred. No. 0.0056;
Matches 51; Conservative 39; Mismatches 95; Indels 30; Gaps 7;
Qy 129 KAVYLHVLPEEPKELMVHVGGLIQMGCVFQSTE-VKHTVKVEWIFSGRRAKEEIVFRYYH 187

Db 28 QAIVVYT-----DREHVGAVGSRVTLHCSFWSSEWSDDISFTWRYQPEGGRDAISIFHYA 83
Qy 188 KLKMSVEYSQSGWHGFQNRVNLVGDIFRNDGSIIMLQGVRESGNYTCSIHLGNLVFKKT- 246
Db 84 K--GQPYIDVGTGFKERIQWGDPRWKDGSIVIHNLIDYSDNGTFTCDVKNPDPDIVGKTS 140
Qy 247 -IVLHVSPPEEPTLVTPAALRPLVLGGNQLVIVGIVCATILLPVLILIVKTKCGNK-- 303
Db 141 QVTLVFEKVTRY-----GVVLGA-----VIGGLVGVVLLLLLLFFVYVRYCWLRRQA 188
Qy 304 -----SSVNSTVLVKNTKTKNPEIKPKCHFRC 332
Db 189 ALQRLSAMEKGLHKPKDQASKRGRTQTPVLYAQC 223

RESULT 7
161783
sodium channel beta 2 subunit - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C:Accession: 161783
R:Isom, L.L.; Ragsdale, D.S.; DeJongh, K.S.; Westenbroek, R.E.; Reber, B.F.X.; Scheuer, J.
Cell 83, 433-442, 1995
A:Title: Structure and Function of the Beta 2 Subunit of Brain Sodium Channels, a Transme
A:Reference number: A57843; MUID:96067641; PMID:8521473
A:Accession: 161783
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-186 <RES>
A:Cross-references: EMBL:U37147; NID:91086498; PIDN:AAB60506.1; PID:g1086499
C:Genetics:
A:Gene: SCN2B
A:Introns: 50/3; 120/2

Query Match 6.4%; Score 132.5; DB 2; Length 186;
Best Local Similarity 28.0%; Pred. No. 0.0043;
Matches 44; Conservative 28; Mismatches 64; Indels 21; Gaps 5;
Qy 27 PPELTIVHVGDSALMGCVFQS--TEDKIFKIDWTLSPEGEAKDHYLYYSN-LSVPIGR 83
Db 6 PTLTSLVNGSDTRLPCTFNSCYTVNHKQFSLNWTYQCSSEEMVLQFRMKIINLKL 65
Qy 84 FQNRVHLMGDILCDNGSLILQDVQADQGYICEI-----RLKGESQVFKKAVLVHLPE 138
Db 66 FGRVFEFGNPSKYDVSVTLNQVLEDEGIYNCVITNPPDRHRHGKIIYIQ-VLLEVPPE 124
Qy 139 EPKELMVHVG-----LIQMGCVFQSTEVK 163
Db 125 RDSIVAVIGASVGGFLAVLVILVMVVKVRRKKEQK 161

RESULT 8
JH0252
myelin P0 protein precursor - human
N:Alternate names: myelin protein zero
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 06-Dec-1996 #text_change 16-Jun-2000
R:Hayaasaka, K.; Nanao, K.; Tahara, M.; Sato, W.; Takada, G.; Miura, M.; Uyemura, K.
Biochem. Biophys. Res. Commun. 180, 515-518, 1991
A:Title: Isolation and sequence determination of cDNA encoding the major structural prote
A:Reference number: JH0252; MUID:92062068; PMID:1719967
A:Accession: JH0252
A:Molecule type: mRNA
A:Residues: 1-248 <HAY>
A:Cross-references: GB:D10537; GB:D90501; NID:9220073; PIDN:BAA01395.1; PID:g220074
R:Hayasaka, K.; Ohnishi, A.; Takada, G.; Fukushima, Y.; Murai, Y.
Biochem. Biophys. Res. Commun. 194, 1317-1322, 1993
A:Title: Mutation of the myelin P0 gene in charcot-marie-tooth neuropathy type 1.
A:Reference number: JN0704; MUID:93356807; PMID:7688964
A:Accession: JN0704
A:Molecule type: mRNA

A;Accession: A57843
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: EMBL:U37036; NID:g1086496; PIDN
C;Genetics:
A;Gene: SCNB2

	Query Match	6.2%; Score 127.5; DB 2; Length 215;
	Best local Similarity	27.4%; Pred. No. 0.012;
	Matches	43; Conservative 28; Mismatches 65; Indels 21; Gaps 5;
Qy	27 PPELTVHVGSALMGCVFQS--TEDKCFIKDWTLSGGEHAKDEVLYYYN-LSVPGR	83
Dd	35 PTTLUSVLNGSDTRUPCTFNSCYTVNHKQFSUNWTFYCENCSCEMFLOFRMKIINLKLR	94
Qy	84 FQNRVHLMDGLICNDGSLLLQQVOEADGTGYICEI-----RLKGESOVFKCAAVLVHLVE	138
Dd	95 FGDRVFSGNSPKYDVSVTLKNVLEDEGIYNCVTITPPDRRHGHGKIYLQ-VLLEVPP	153
Qy	139 EPKELMVHG-----LIQMGCVFQSTEVK	163
Dd	154 RDSFTVAIVIGASVGGFIAWLILVMWKVCVRKKKEOK	190

RESULT 12
A53449
plasmatocytoma-associated neuronal glycoprotein PANG - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 24-Sep-1999
C:Accession: A53449
P:Connolly, M.A.; Grady, R.C.; Mushinski, J.F.; Marcu, K.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 1337-1341, 1994
A:Title: PANG, a gene encoding a neuronal glycoprotein, is ectopically activated by intracerebral injection of a neurotrophic factor
A:Reference number: A53449; MUID:94151325; PMID:8108413
A:Accession: A53449
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1028 <CON>
A:Cross-references: GB:I01991; NID:g200056; PIDN:AAAL17403.1; PID:g200057
C:Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology
C:Keywords: glycoprotein

Query Match	6.1%;	Score 126;	DB 2;	Length 1028;
Best Local Similarity	20.3%;	Pred. No. 0.11;		
Matches	57;	Conservative 49;	Mismatches 91;	Indels 84; Gaps 14;
QY	17	SLGLNDLNVSPPELTVHVGDSALMGC-----VFQSTEDKCI FKI-DWTLSRGEHAKD	67	
Db	370	ALTITNLNV-----DSGMFQCIAENKHGLIYSAEUKVVASAFDFSRNPKMKVQV	420	
QY	68	EYV-----LYYYSNLSPICRFQRNRLHMGDILNCDSGLLLQDVQBGADQ	111	
Db	421	VQVGSILVLDCKPRASPRALSPFWKKGDMMV-REQARVSFL-----NQGGLIKMNVTKADA	474	
QY	112	GTYICEIRLKGESQVFKKAVLHVLPEEPKELM-----VHVUGLIQMCGVCFQSTEVKX	164	
Db	475	GTYYC-----IAENQFGRANGTHLVVTEPTILLAPSNMVDVAGESVILPC-----QVQH	525	
QY	165	VTKVE-----WTFSGRRAKEIVFRRYHKLRMVSVEYSQSWGHQFNRNVLGVDFIRNDGSIM	220	
Db	526	DPLLEDIMFAWYFNG-----ALTDFFKDGSHFEK-----VGG-SSSGDLM	563	
QY	221	LQGVRESDDGNYTCSIHLG--NLVFKKTVILHVSPEEPRTL	259	
Db	564	IRNIQLKHSRGYVCWQVGTGVDVSASAALIIVRGSPGPPENV	604	

RESULT 13

SHP substrate-1 protein, 509 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Apr-1997 #sequence revision

C;Accession: JC5288
C;Yamamoto, T.; Matoraki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.; Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A;Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization
A;Reference number: JC5287; MUID:97223399; PMID:9070220
A;Contents: Brain
A;Accession: JC5288
A;Molecule type: mRNA
A;Residues: 1-509 <YAM>
A;Cross-references: DBJ:D87967; NID:G1864012; PIDN:BA413520,1; PID:G1864013
C;Comment: This protein is a glycosylated receptor-like protein and plays a role in cell acts as a docking protein and induce translocation of SHP-2 from the cytosol to the plasma
C;Genetics:
A;Gene: shps-1
A;Map position: 2

Query Match	6.1%;	Score 125.5;	DB 2;	Length 509;
Best Local Similarity	21.2%;	Pred. No. 0.05;		
Matches 105;	Conservative 64;	Mismatches 162;	Indels 165;	Gaps 24;

Qy	4	PLKLILLPVLLDVS	LGI--	NDLVNSPPELT	THV--	GDSALMGCVFQSTED	KCI	KIDWTL	59
				:	:		:	:	
				:	:		:	:	
Db	13	PLLLCLLSASC	FC	TGVTGKEL	KVTP	PEKSVS	VAA	GDSTVLNCT	LTSLLP--
				:	:		:	:	
				:	:		:	:	
Qy	60	SPGEHAXDEV	LVYYLSN	LSPIGR	FORVHLM	GM	LICN--	DGSLILD	VQEA
		:	:	:	:	:	:	:	
		:	:	:	:	:	:	:	
Db	71	GVGO---	SRLLI	YSFTGE	HPF----	RVTNV	SDATK	RNNMDF	SIRISNV
		:	:	:	:	:	:	:	
		:	:	:	:	:	:	:	
Ov	117	-----	ETRLK	GESOV	-----				126

RESULT 14
A57638
receptor tyrosine kinase egl-15 precursor - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 24-Sep-1999
C/Accession: A57638
R; DeVore, D.L.; Horvitz, H.R.; Stern, M.J.
Cell 83, 611-620, 1995
A/Title: An FGF receptor signaling pathway is required for the normal cell
A/Reference number: A57638; MUID:96069862; PMID:7585964

A;Accession: A5/638
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1040 <DEV>
A;Cross-references: GB:U39761; NID:g1079711; PIDN:AAC46934.1; PID:g1079712
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases: protein kinase homologs

C;Keywords: ATP
F:638-935/Domain: protein kinase homology <KIN>
F:646-654/Region: protein kinase ATP-binding motif

Query Match 6.1%; Score 125.5; DB 2; Length 1040;
Best Local Similarity 19.9%; Pred. No. 0.12;
Matches 85; Conservative 73; Mismatches 150; Indels 119; Gaps 23;

QY 15 DYSL-----GLNDLNV-----PPELTVHVGDSSALMGCVFQSTEDKCFKIDWTLSPGE 63
DB 263 DYSVQVPADAGLTGELNITAEPP-----YFKSNDNIIVLFNETHALPAGR 308
QY 64 HAK-----DEYVLYYSN-----LSVPIGRFQNRVHLMGDIILCNDGSLLLQDVQEA 109
DB 309 TLKLNCRAGVPEPQIIWYKNGKMLKKSARSGGYEFK-----NRWSLEVEDAVVA 360
QY 110 DQGTVCIRLK-GESQVFKKAVLVH-----VLPEPKELMVHVGLIQMGCVFQSTE 161
DB 361 DSGEFHCEALNKVGSARKYFHVIIIVNRMRPPIIVPNILANQSVNINDTATFCHKVSD 420
QY 162 VKHVTKEWIFSGRRAKEEIVFRYYHKLMSVEYSQSNGHFQN-----RVNLVGDIFRNDG 217
DB 421 LPHII---WV---RINKINGSYSYN--NSAEYMFNTYEMDTPDKAHVHVGD----ES 468
QY 218 SIMLQGVRESGGNYTC-----SIHLGNLVFKKTIIVLH-VSPEEPT-----LV 260
DB 469 TLTIFNVSLDQGIYACLSGNSLGMANATLTVNEFMAIHLLTGDEPKIDRWTTSDYIF 528
QY 261 TPAALRPLVLGNGQLVIIVGIVCATILLPLVILIVKTCGNKSSVNSTV-LVKNTKTN 319
DB 529 T-----TILLFLLAAT--LFGILFMVCKQTLHKKGFMDDTVGLVARKKRV- 572
QY 320 PEIKEKPCCH--PERCEGEKHIY-----SPIIVREVIIEEPESEKSEATYTMH-----P 366
DB 573 -VWSKRPWNEDNENSDDPSYPYQIQIETPTITKEAARKQKRMNSENTVLSEYEVDSDP 631
QY 367 WMPSLRS 373
DB 632 VWEVERS 638

RESULT 15
T22889
hypothetical protein F58A3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T22889
R;Lennard, N.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19632
A;Accession: T22889
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1103 <WIL>
A;Cross-references: EMBL:Z81017; PIDN:CAB02673.1; GSPDB:GN00028; CESP:F58A3.2
A;Experimental source: clone F58A3
C;Genetics:
A;Gene: CESP:F58A3.2
A;Map position: X
A;Introns: 30/1; 50/3; 104/3; 128/1; 245/3; 323/3; 403/3; 457/3; 493/3; 639/2; 665/3; 76
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 6.1%; Score 125.5; DB 2; Length 1103;
Best Local Similarity 19.9%; Pred. No. 0.13;
Matches 85; Conservative 73; Mismatches 150; Indels 119; Gaps 23;

QY 15 DYSL-----GLNDLNV-----PPELTVHVGDSSALMGCVFQSTEDKCFKIDWTLSPGE 63
DB 263 DYSVQVPADAGLTGELNITAEPP-----YFKSNDNIIVLFNETHALPAGR 308
QY 64 HAK-----DEYVLYYSN-----LSVPIGRFQNRVHLMGDIILCNDGSLLLQDVQEA 109
DB 309 TLKLNCRAGVPEPQIIWYKNGKMLKKSARSGGYEFK-----NRWSLEVEDAVVA 360

Search completed: October 1, 2004, 21:07:31
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2004, 20:51:10 ; Search time 25 Seconds
(without alignments)
820.626 Million cell updates/sec

Title: US-09-989-728-422
Perfect score: 2067
Sequence: 1 MFCEPLKLLPVLDDYSLGL.....RNSLEKKGSGGMPKTOQAF 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	168	8.1	365	1	CXAR HUMAN
2	146.5	7.1	246	1	MYPO HETER
3	146	7.1	365	1	CXAR MOUSE
4	140.5	6.8	249	1	MYPO CHICK
5	138.5	6.7	215	1	CIB2 HUMAN
6	137	6.6	215	1	EVAL MOUSE
7	137	6.6	338	1	LAMP HUMAN
8	135	6.5	338	1	LAMP RAT
9	133	6.4	686	1	IPL2 MOUSE
10	132	6.4	248	1	MYPO HUMAN
11	131	6.3	219	1	MYPO BOVIN
12	131	6.3	248	1	MYPO MOUSE
13	130	6.3	248	1	MYPO RAT
14	128.5	6.2	319	1	A33 HUMAN
15	128	6.2	686	1	IPL2 HUMAN
16	127.5	6.2	215	1	CIB2 RAT
17	127	6.1	316	1	FCGA PANTR
18	125.5	6.1	1040	1	EG15 CAEL
19	123.5	6.0	285	1	FCG2 RAT
20	123.5	6.0	595	1	SILL HUMAN
21	123.5	6.0	1363	1	VGR3 MOUSE
22	122.5	5.9	338	1	LAMP CHICK
23	120.5	5.8	597	1	SILL PANTR
24	119	5.8	696	1	IPL1 HUMAN
25	119	5.8	696	1	IPL1 PANTR
26	119	5.8	764	1	IPL1 HUMAN
27	118.5	5.7	317	1	FCGA HUMAN
28	118.5	5.7	1298	1	VGR3 HUMAN
29	118	5.7	333	1	ANAL DROME
30	118	5.7	898	1	FAS2 SCHAM
31	117.5	5.7	215	1	EVAL HUMAN
32	116.5	5.6	513	1	SHS1 MOUSE
33	116	5.6	695	1	IPL1 MOUSE

ALIGNMENTS

RESULT 1

ID	CXAR HUMAN	STANDARD;	PRT;	365 AA.
AC	F78310; O00694;			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-adenovirus receptor) (hCAR) (CVB3 binding protein).			
DE	adenovirus receptor			
GN	CXADR OR CAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[8]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[9]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[10]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[11]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[12]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[13]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[14]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[15]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[16]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[17]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[18]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[19]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[20]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[21]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[22]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[23]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[24]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[25]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[26]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[27]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[28]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[29]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[30]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[31]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[32]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[33]			
RP	SEQUENCE FROM N.A.			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W., "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			

O60469 homo sapien
Q9xt56 bos taurus
Q9nyz4 homo sapien
P59824 rattus norv
P98160 homo sapien
Q90773 gallus gall
P97798 mus musculu
P21995 mus musculu
Q8hxj7 macaca fasc
Q9p2b2 homo sapien
O94856 homo sapien
Q9ny72 homo sapien

34 116 5.6 2012 1 DSCA HUMAN
35 115.5 5.6 298 1 JAMI_BOVIN
36 115.5 5.6 499 1 SILL_HUMAN
37 115 5.6 696 1 IPL1 RAT
38 113.5 5.5 4391 1 PGBM_HUMAN
39 112 5.4 353 1 CPU_CHICK
40 112 5.4 1493 1 NEO1_MOUSE
41 110.5 5.3 330 1 EMB_MOUSE
42 110 5.3 215 1 CIB3_MACFA
43 109.5 5.3 879 1 FRP_HUMAN
44 109.5 5.3 1240 1 NFAS_HUMAN
45 109 5.3 215 1 CIB3_HUMAN

34 116 5.6 2012 1 DSCA HUMAN
35 115.5 5.6 298 1 JAMI_BOVIN
36 115.5 5.6 499 1 SILL_HUMAN
37 115 5.6 696 1 IPL1 RAT
38 113.5 5.5 4391 1 PGBM_HUMAN
39 112 5.4 353 1 CPU_CHICK
40 112 5.4 1493 1 NEO1_MOUSE
41 110.5 5.3 330 1 EMB_MOUSE
42 110 5.3 215 1 CIB3_MACFA
43 109.5 5.3 879 1 FRP_HUMAN
44 109.5 5.3 1240 1 NFAS_HUMAN
45 109 5.3 215 1 CIB3_HUMAN

34 116 5.6 2012 1 DSCA HUMAN
35 115.5 5.6 298 1 JAMI_BOVIN
36 115.5 5.6 499 1 SILL_HUMAN
37 115 5.6 696 1 IPL1 RAT
38 113.5 5.5 4391 1 PGBM_HUMAN
39 112 5.4 353 1 CPU_CHICK
40 112 5.4 1493 1 NEO1_MOUSE
41 110.5 5.3 330 1 EMB_MOUSE
42 110 5.3 215 1 CIB3_MACFA
43 109.5 5.3 879 1 FRP_HUMAN
44 109.5 5.3 1240 1 NFAS_HUMAN
45 109 5.3 215 1 CIB3_HUMAN

RA Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helcon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Greven E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC or send an email to license@isb-sib.ch).
DR EMBL; Y07593; AAC68868.1; -
DR EMBL; U07116; AAC51234.1; -
DR EMBL; AF169366; AAF05908.1; -
DR EMBL; AF169366; AAF05908.1; JOINED.
DR EMBL; AF169361; AAF05908.1; JOINED.
DR EMBL; AF169362; AAF05908.1; JOINED.
DR EMBL; AF169363; AAF05908.1; JOINED.
DR EMBL; AF169364; AAF05908.1; JOINED.
DR EMBL; AF169365; AAF05908.1; JOINED.
DR EMBL; AF200465; AAF24344.1; -
DR EMBL; AF242865; AAG01088.1; -
DR EMBL; AF242862; AAG01088.1; JOINED.
DR EMBL; AF242864; AAG01088.1; JOINED.
DR EMBL; BC003684; AAH03684.1; -
DR EMBL; BC010536; AAH10536.1; -
DR PDB; 1E4J; 13-JUL-01.
DR PDB; 1F5W; 08-NOV-00.
DR PDB; 1KAC; 24-NOV-99.
DR Genew; HGNC:2559; CXADR.
DR MIM; 602621; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 365
FT DOMAIN 20 237
FT TRANSMEM 238 258
FT POTENTIAL 258
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE 1.
FT IG-LIKE C2-TYPE 2.
FT BY SIMILARITY.
FT DISULFID 162 212
FT CARBOHYD 106 106
FT CARBOHYD 201 201
SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FE64 CRC64;

Query Match

8.1%; Score 168; DB 1; Length 365;

Best Local Similarity 21.8%; Pred. No. 2e-06;
Matches 87; Conservative 65; Mismatches 148; Indels 100; Gaps 18;
QY 5 LKLLPVLVLLDYSGLNDLVNPPDLTVH--VGDALMGCVFQ-STEDKCFKIDWTLSLP 61
Db 5 LCFVLLCGWDFP---RSLSTTTPEEMTEKARGETAYLPCKFTLSPEQGPDLIEWLSP 61
QY 62 GEHAKDEVLYYNSLSPIGRF---QNRVHL-MGDILCNDGSLLLQDVQADQTYICE 117
Db 62 ADNQKVDQVILYSGDKIYDDYIPDLKGRVHTSNDLSGASINVTNLQSLDITGYQCK 121
QY 118 IRLGESQVFKKAVVLVHLVPEPEKELMVHVGGLIQMGCVF-----QSTEVKHKVKEWIFPS 173
Db 122 V--KKAPGVANKIHLVVL-VKPSGARCVCVDSSEIGSDFKIKCKPKESGLPLQYEW-- 175
QY 174 GRRAKBEIVFRYHYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLQGVRESGGNYT 233
Db 176 -----QKLSDSQKMPSTW-----LAEMTSSV-----ISVKNASSEYSGTYS 211
QY 234 CSIHGLNLVFKKTVLHVSPPEPRTLVTPAALRPLVLGNGNLVIVGIVCATILLPLVLI 293
Db 212 CTVR--NRVGSQCLLRUNVVP-----SNKAGLIAGAILGTLALALIG 254
QY 294 LIVKKTGKNSVNSVTLVQNTKTNPEIKPKCHPERCEGKHIYSPPIVREIEEPEP 353
Db 255 LII-FCC-----RKEREKYEKEVHHD-----IREDVP 282
QY 354 SEKSEATYMTMHPVWPSPRSRDN--SLEKSGGGMPKQ 391
Db 283 PPKSTSTARSY-----IGSNHSLGSMSPSNMEGYSKTQ 317
RESULT 2
ID MYPO_HETPR STANDARD; PRT; 246 AA.
AC P20938;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
DE protein) (MPP).
OS Heterodontus francisci (Horn shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Heterodontidae; Heterodontiformes;
OC Heterodontidae; Heterodontus.
OX NCBI_TaxID=7792;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90040744; PubMed=2478717;
RA Saavedra R.A., Fors L., Aebersold R.H., Arden B., Horvath S.,
RA Sanders J., Hood L.;
RT "The myelin proteins of the shark brain are similar to the myelin
RT proteins of the mammalian peripheral nervous system.";
RL J. Mol. Evol. 29:149-156(1989).
CC -!- FUNCTION: Creation of an extracellular membrane face which guides
CC the wrapping process and ultimately compacts adjacent lamellae.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Found only in peripheral nervous system
CC Schwann cells.
CC -!- PTM: N-GLYCAN IS SULFATED (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Belongs to the myelin P0 protein family.
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CC EMBL; X16714; CAB37865.1; -


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DR PIR; A32999; A32999.
DR HSP; P06907; 1NEU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig.V.
DR PRINTS; IPR000920; MYELIN_P0.
DR SMART; PR00213; MYELINP0.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00568; MYELIN_P0; 1.
DR MYELIN; Structural protein; Glycoprotein; Transmembrane;
KW Phosphorylation; Immunoglobulin domain; Signal.
FT SIGNAL 1
FT CHAIN 27
FT DOMAIN 28 246
FT TRANSMEM 28 150
FT DOMAIN 151 178
FT DOMAIN 179 246
FT DOMAIN 28 143
FT DISULFID 48 125
FT CARBOHYD 120 120
SQ SEQUENCE 246 AA; 27335 MW; A776A9ED9D430FA0 CRC64;

Query Match 7.1%; Score 146.5; DB 1; Length 246;
Best Local Similarity 26.0%; Pred. No. 7e-05;
Matches 44; Conservative 37; Mismatches 61; Indels 27; Gaps 6;

QY 147 VGGILQMCVQFQSTE-VKHVTKVEIFSGRRAKEI-VFYYHKLKMSVEYSQSGHFQ 204
DB 40 VGSVDVTLVCGFWSNVEYSDLTLSWFRPDRSDIISIFHYGN----GVPIERKMGQRF 95
QY 205 RVNLVGLDFRNDGSIIMQGVRESQDGNVTCSTHGLNGLVFKKTVLHVSPPEPRTLVT 264
DB 96 RVEWVGDISKEDSGSIVRNLDYDNGTCTCDKVPDPVVGTSDDVHLVYD-----K 147
QY 265 LRPLVGLNQVLVIIVGIVCATILLPVLL-----IVKTCGNKSS 305
DB 148 IPPVGAG-----VMSGAIIGTFLGILLVGLVLFYRIVRRARSETS 191

RESULT 3
CXAR MOUSE STANDARD; PRT; 365 AA.
AC P97792; O09052;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cocksackievirus and adenovirus receptor homolog precursor (mCAR).
GN CXADR OR CAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Horwitz M.S.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Cocksackie B viruses and
RT adenoviruses 2 and 5."
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/MAI;
RX MEDLINE=97250541; PubMed=9096397;
RA Tomko R.P., Xu R., Philipson L.;
RT "HCAR and mCAR: the human and mouse cellular
RT adenoviruses and group B cocksackieviruses."
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX STRAIN=98080429; PubMed=9420240;

RA Bergelson J.M., Krithivas A., Celi L., Droguett G., Horwitz M.S.,
RA Wickham T., Crowell R.L., Finberg R.W.;
RT "The murine CAR homolog is a receptor for cocksackie B viruses and
RT adenoviruses."
RL J. Virol. 72:415-419(1998).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC
DR EMBL; Y10320; CAA71368.1; -.
DR EMBL; U0715; AAC53148.1; -.
DR EMBL; Y11929; CAA72679.1; -.
DR MGD; MGI:1201679; Cxadr.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SMO0408; IGC2; 1.
DR PROSITE; PS00835; IG LIKE; 2.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat.
FT SIGNAL 1
FT CHAIN 20 365
FT DOMAIN 20 237
FT TRANSMEM 238 258
FT DOMAIN 259 365
FT DOMAIN 20 136
FT DOMAIN 141 228
FT DISULFID 41 120
FT DISULFID 162 212
FT CARBOHYD 106 106
FT CARBOHYD 201 201
FT CONFLICT 340 365
SQ SEQUENCE 365 AA; 39947 MW; 544594B52A34B2A2 CRC64;

Query Match 7.1%; Score 146; DB 1; Length 365;
Best Local Similarity 21.8%; Pred. No. 0.00013;
Matches 87; Conservative 58; Mismatches 155; Indels 100; Gaps 18;

QY 5 LKILLPVLLDYSGLNDLNVSPPELVH--VGDSALMGCVFQ-STEDKCFIKIDWTLSP 61
DB 5 LCFVLLCGIADFTSG---LSITTPQRIEXAKGETAYLPCKFTLSPEQDGLDIENLSP 61
QY 62 GEHAKDEVLYYNSNLSPVIGRF---QNRVHL-MGDLNCGSLLLQVQADQTYICE 117
DB 62 SDNQIVDQVILYSGDKIYDNYYPDLKGRVHFTSNDVKSGDASINVNLQLSDIGTYQCK 121
QY 118 IRLKGEQVFKKAVLVHLPPEPKELMVHVGGLLQMGCVF---QSTEVKHVTKVEWTFPS 173
DB 122 V--KKAPGVANKKFLLV-LVKPSGTRCFVDGSGSEIGNDFKLCKEPEKSGSLPQFEW--- 175
QY 174 GRRAKEEIVFYYHKLKMSVEYSQSGWGFQNRVNLVGLDIFRNDGSIIMQGVRESQDGNV 233
DB 176 -----QKLSDSQTMPTPW-----LAETSPV-----ISVKNASSSEYSGTYS 211
QY 234 CSHLGNLVFKKTVLHVSPPEPRTLVTPAALRPLVGLGNQVLVIIVGIVCATILLPVLI 293
DB 212 CTVQ--NRVSGDQCMRLDVLVPP-----SNRAGTIAGAVIGTLLAL-VLI 253
QY 294 LIVKTCGNKSSVNSTVLVKNKTNTEIKEKPCHECEKEKHIYSPVIVREVIEEEP 353
DB 254 GAILFCC-----HRXREEKEVEVHHD-----IREDPV 282
QY 354 SEKSEATYMTMHPVWPSLRSDRNN--SLEKKSGGMPKQTQ 391
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CC -!- TISSUE SPECIFICITY: Brain specific.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
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CC -----
DR EMBL; AF007783; AAC26013.1; -
DR EMBL; AF049498; AAC05274.1; -
DR EMBL; AF049497; AAC05208.1; -
DR EMBL; AF049496; AAC05208.1; JOINED.
DR EMBL; U87555; AAF21472.1; -
DR EMBL; AF107028; AAD47196.1; -
DR EMBL; BC036793; AAH36793.1; -
DR EMBL; HGNC:10589; SCN2B.
DR MIM; 601327; -
DR GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
DR GO; GO:0006814; P:sodium ion transport; TAS.
DR GO; GO:0007288; P:synaptic transmission; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR000920; Myelin_P0.
DR PRINTS; PR00213; MYELIN_P0.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Signal; Immunoglobulin domain; Sodium channel.
FT SIGNAL 1 29
FT CHAIN 30 215
FT DOMAIN 30 159
FT TRANSMEM 160 180
FT DOMAIN 181 215
FT DOMAIN 32 154
FT DISULFID 55 127
FT CARBOHYD 42 42
FT CARBOHYD 66 66
FT CARBOHYD 74 74
FT CONFLICT 2 2
FT CONFLICT 8 8
FT CONFLICT 15 15
FT CONFLICT 48 48
FT CONFLICT 68 68
FT CONFLICT 156 156
FT CONFLICT 178 179
SQ SEQUENCE 215 AA; 24326 MW; 94A30A60A32683F3 CRC64;

Query Match 6.7%; Score 138.5; DB 1; Length 215;
Best Local Similarity 29.2%; Pred No. 0.00027;
Matches 47; Conservative 25; Mismatches 60; Indels 29; Gaps 6;

Qy 27 PPELVTHVGDALMGCVFQS--TEDKCFIKIDWTLSPGEGHAKDEYLYYGN--LSVPTGR 83
Db 35 PATLVNLGSDARLPCTFNCSVTYVNHKQSLNWTYQECNCSSEMFQPRMKINLKLER 94
Qy 84 FQNRVHLMGDLICNDGSLLLQDVQADQGTICEI-----RLKGESQVFKKAVLVHLVPE 138
Db 95 FQDRVEFGSPSKYDVSVMLENVQPEDEGIYNCYIMNPPDRHRGHGKI-----LQVLME 149
Qy 139 EPKE-----LMVHVG-----LIQMGCVFQSTEVK 163
Db 150 EPPERDSTAVIVGASGGFLAVLVLMVVKVRRKKEQK 190

RESULT 6
ID_EVAL MOUSE
AC O70255;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Epithelial V-like antigen 1 precursor.
GN EVAL OR EVA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAG-2; TISSUE=Thymus;
RX MEDLINE=98252857; PubMed=9585423;
RA Guttlinger M., Sutti F., Panigada M., Porcellini S., Merati B.,
RA Mariami M., Teesalu T., Consalez G.G., Grassi F.;
RT "Epithelial V-like antigen (EVA), a novel member of the immunoglobulin
RT superfamily, expressed in embryonic epithelia with a potential role as
RT homotypic adhesion molecule in thymus histogenesis.";
RL J. Cell Biol. 141:1061-1071(1998).
CC -!- FUNCTION: Mediates homophilic cell-cell adhesion.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Expressed in liver and gut, skin, and testis
CC but not in thymocytes, lymphocytes, macrophage or dendritic cells
CC or cell lines.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC -----
DR EMBL; AF030454; AAC40128.1; -
DR HSP; P06907; INEU.
DR MGD; MGI:1289160; Eva.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR000920; Myelin_P0.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR00213; MYELIN_P0.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Cell adhesion; Immunoglobulin domain; Transmembrane; Glycoprotein;
KW Signal.
FT SIGNAL 1 26
FT CHAIN 27 215
FT DOMAIN 27 154
FT TRANSMEM 155 175
FT DOMAIN 176 215
FT DOMAIN 27 141
FT DISULFID 47 123
FT CARBOHYD 39 39
FT CARBOHYD 118 118
SQ SEQUENCE 215 AA; 24162 MW; F6E5E36787CE69D5 CRC64;

Query Match 6.6%; Score 137; DB 1; Length 215;
Best Local Similarity 27.1%; Pred No. 0.00036;
Matches 57; Conservative 33; Mismatches 92; Indels 28; Gaps 9;

Qy 8 ILLPVLLDYSILGLNDLVNPSPELLVHVGDSALMGCVFQSTEDKCFK-----IDW 57
Db 8 LVLPPLL--SLQTLAL--CPTAEVITYSGALEAVNGTDVRLKCTFSSFPVPGDALTVTW 63
Qy 58 TLPFGEHAKDEYLYYYSNLSVPT-GRFQNRVHLMGDLICNDGSLLLQDVQADQGTIYC 116
Db 64 NFRPRDGRSQFVFYHMDPPRPMGSRFKDRVVDGNPERYDVSILLWKLFQDDNGTYTC 123
Qy 117 EIR-----LKGESQVFKKAVLVHLVPEEPKELMVHVGGLIQMGCVFQSTEV--KHVTKE 169
Db 124 QVKNPPDVGVLGVTIRLSV-HTVPFSEIYFLAIGSACALMIIVVVVLFQHFRRK 182
Qy 170 WI-----FSGRRAKEEIVFRYYHKLRMSVE 194

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CC -----
DR EMBL; U31554; AAA86120.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00408; IGc2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
FT Repeat; Signal; Lipoprotein.
FT SIGNAL 1 28
FT CHAIN 29 315
FT -----
FT LIMBIC SYSTEM-ASSOCIATED MEMBRANE
FT PROTEIN.
FT PROPEP 316 338
FT DOMAIN 29 122
FT IG-LIKE C2-TYPE 1.
FT DOMAIN 132 214
FT IG-LIKE C2-TYPE 2.
FT DOMAIN 219 304
FT IG-LIKE C2-TYPE 3.
FT DISULFID 53 111
FT POTENTIAL.
FT DISULFID 153 197
FT POTENTIAL.
FT DISULFID 239 290
FT POTENTIAL.
FT CARBOHYD 40 40
FT N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 66 66
FT N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 136 136
FT N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 148 148
FT N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 279 279
FT N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 287 287
FT N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 300 300
FT N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 315 315
FT N-LINKED (GLCNAC . .) (POTENTIAL).
FT LIPID 315 315
FT GPI-anchor amidated asparagine
FT (Potential).
FT SEQUENCE 338 AA; 37324 MW; 0B76AFDD68A39BB6 CRC64;
Query Match 6.5%; Score 135; DB 1; Length 338;
Best Local Similarity 19.8%; Pred No. 0.00095;
Matches 71; Conservative 55; Mismatches 123; Indels 110; Gaps 14;
Qy 4 PLKLLPLVLLDYSIGLN--DLNVSPPELTIVHVGDSALMGCVFQSTEDK-----CIF 53
Db 13 PLVLLRLLLPTGLPVRSDVFNRTGDTNITVRQDITAILRCVVEDKNSKVAWLNRSGIIF 72
Qy 54 --KIDWTLSPEHAKDEVLYVYNSLVPIGRFQNRVHLMGDILCNDGSLLLQDVQERADQ 111
Db 73 AGHDKWSLDRPVELEKRALEY-----SLRIQKVDVYDE 106
Qy 112 QTYICEIRLKGESQVFKKAVVLHVLPE--BPKELMVHVGGLIOMGCVFQSTEV-----K 163
Db 107 GSYTCVQTQHEPKTSQVYLIVQPPKLSNITSSDVTNVEGNVTLVCNAGRPEPVITWR 166
Qy 164 HVTKEVWTFSGR-----RAKEEIVFRYHKLKMSVEY-----SQS 198
Db 167 HLTPLGREFEGEEYLEILGITREQSGKVECKAANEVSSADVQKVVTWVYPPITTESKS 226
Qy 199 -----WGHFQNRVNLVG--DIFRNDG--SIMLQGVRESGG 230
Db 227 NEATTGRQASLKCEASAVPAPDFWYRDDTRINSANGLEIKSTEQSSSLTNTVNTTEHYG 286
Qy 231 NYTCSIHLGNLVFKKTVLHVSPPEPRLTVLPAALPLVLGNGNOIIVGVICATILL 289
Db 287 NYTC-----VAANKLGVTNAS-----LVLFPRGVSVRG--INGSISLAVPLWLLAASLPCL 334
RESULT 9
ID IPL2 MOUSE STANDARD; PRT; 686 AA.
AC Q9ERS6; Q9ERS6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
```

```
DE X-linked interleukin-1 receptor accessory protein-like 2 precursor
DE (ILIRAPD-2 related protein) (TIGIRR-1).
GN ILIRAPD2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain, and Liver;
RX MEDLINE=20459050; PubMed=10882729;
RA Born T.L., Smith D.E., Garka K.E., Renshaw B.R., Bertles J.S.,
RA Sims J.E.;
RT "Identification and characterization of two members of a novel class
RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R-related proteins based on signaling.";
RT J. Biol. Chem. 275:29946-29954 (2000).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=21472256; PubMed=11587848;
RA Ferrante M.I., Ghiani M., Bulfone A., Franco B.;
RT "ILIRAPL2 maps to Xq22 and is specifically expressed in the central
RT nervous system.";
RT Gene 275:217-221 (2001).
RL -- SUBCELLULAR LOCATION: Type I membrane protein.
CC -- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9ERS6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9ERS6-2; Sequence=VSP_008056, VSP_008057;
CC Note=may be due to an intron retention;
CC -- TISSUE SPECIFICITY: Detected in fetal brain after day 12.5, in
CC particular in parts of the diencephalon and in the basal plate of
CC the spinal cord. In postnatal brain detected in cerebral cortex,
CC olfactory bulb, in the CA1 region of the hippocampus and in
CC Purkinje cells of the Xth cerebellar lobule.
CC -- SIMILARITY: Belongs to the interleukin-1 receptor family.
CC -- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -- SIMILARITY: Contains 1 TIR domain.
CC -----
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EMBL; AF284437; AAG21371.1; -.
EMBL; AJ277831; CAC10559.1; -.
MGD; MGI:1913106; Ilirap2.
InterPro; IPR007110; IG-like.
InterPro; IPR003599; IG.
InterPro; IPR004075; IL1_receptor1.
InterPro; IPR004077; IL1_receptor1p.
InterPro; IPR000157; TIR.
Pfam; PF00047; ig; 3.
Pfam; PF01582; TIR; 1.
PRINTS; PR01539; INTRLEUKINR2.
PRINTS; PR01337; INTRLEUKINR1F.
SMART; SM00409; IG; 2.
SMART; SM00255; TIR; 1.
PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS50104; TIR; 1.
Receptor; Repeat; Signal; Transmembrane; Immunoglobulin domain;
KW Glycoprotein; Alternative splicing.
FT SIGNAL 1 16
FT CHAIN 17 686
FT DOMAIN 17 354
FT TRANSMEM 355 375
FT POTENTIAL.
FT X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY
FT PROTEIN-LIKE 2.
FT EXTRACELLULAR (POTENTIAL).
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FT DOMAIN 376 686 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 132 IG-LIKE C2-TYPE 1.
FT DOMAIN 141 232 IG-LIKE C2-TYPE 2.
FT DOMAIN 239 347 IG-LIKE C2-TYPE 3.
FT DOMAIN 400 559 TIR.
FT DISULFID 53 116 POTENTIAL.
FT DISULFID 162 214 POTENTIAL.
FT DISULFID 265 331 POTENTIAL.
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 328 328 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 350 354 DLYK -> GILFS (in isoform 2).
FT VARSPLIC 355 686 /FTID=VSP 008056.
FT VARSPLIC 355 686 Missing (in isoform 2).
SQ SEQUENCE 686 AA; 78797 MW; 36160D1CDE9B8264 CRC64;

Query Match 6.4%; Score 133; DB 1; Length 686;
Best Local Similarity 20.4%; Pred. No. 0.0035;
Matches 78; Conservative 60; Mismatches 130; Indels 114; Gaps 18;

QY 38 ALMGCVFQSTEDKCIKFK-----IDWTLS-----PGEHAKDEVLYY-----YS-- 75
DB 8 ALVVCASVSTNLKMKVSKNSVDGCDWSDVLTXYMALAGEPVVRKCALFYIRTNYSWA 67

QY 76 NLSVPIGRFQNRVHLMGDILCN-----DGLLLQDVQEQADQGYTCIEILKLGESQVF 127
DB 68 QSTGLRLMWYRKGLDEPIIFSEVRMSKEEDAIWFHSABEQDSQGYFTCVLR--NSTYCM 125

QY 128 KKAIVLHVLPEPKELMHVHGLIQMGCVFQS-----TEVKHYTKVEWI-----PSGR 176
DB 126 KVSMSLTVAENE-----SGLCYSRIRYLEKSEVTKRKEISCPDMDFFKSD 172

QY 177 AKKEITVFYHYHKLMSVEYSQSWGHGFQNRVNLVGDIFRDGDSIMLQGVRESQGNVTC 236
DB 173 QEPDVVWYKECKPKM-----WRSI-----LIQKNALLIQEVEEDGGNYTC 216

QY 237 HGNLVFKKTIIVHVSPEPRTLVTPAALRPLVLGNQNLVII-----VGIVCATILL 289
DB 217 KYEGKLVRTTELKVT-----ALLTDKPKPLFPMEQPSVDIVQLGKPLNIPCKAFFG 271

QY 290 -----PVL-----LIIVKTKGNSVNSVTLVKNKTNTPEIKE 324
DB 272 SSGSPMIYWMKGEKFIIELAGHIREGEIRLLKEHLGEX-EVELTLIFDSV--VEADLAN 328

QY 325 KPCHFERCEGKHYSPIITVRE 346
DB 329 YTCHEVNRNKRKH--ASVLLRK 348
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RESULT 10
MYP0 HUMAN STANDARD; PRT; 248 AA.
AC P25189; Q16072; Q92677; Q9B967;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
DE protein) (MPP).
GN MPZ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=92062068; PubMed=17119967;
RA Hayasaka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,
RA Uyemura K.;
RT "Isolation and sequence determination of cDNA encoding the major
RT structural protein of human peripheral myelin.";
```

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RL Biochem. Biophys. Res. Commun. 180:515-518(1991).
[2]
RP SEQUENCE FROM N.A., AND VARIANT CMT1B HIS-98.
RC TISSUE=spinal cord;
RX MEDLINE=93356807; PubMed=7688964;
RA Hayasaka K., Ohnishi A., Takada G., Fukushima Y., Murai Y.;
RT "Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy
RT type 1.";
RL Biochem. Biophys. Res. Commun. 194:1317-1322(1993).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94154677; PubMed=7509228;
RA Phan-Dinh D., Fourbil Y., Blanquet F., Mattei M.-G., Roeckel N.,
RA Latour P., Chazot G., Vandenbergh A., Dautigny A.;
RT "The major peripheral myelin protein zero gene: structure and
RT localization in the cluster of Fc gamma receptor genes on human
RT chromosome 1q21.3-q23.";
RL Hum. Mol. Genet. 2:2051-2054(1993).
[4]
RP SEQUENCE FROM N.A.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSS in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RP SEQUENCE OF 24-248 FROM N.A.
RA Nellis E., Timmerman V., De Jonghe P., Muylle L., Martin J.-J.,
RA Van Broeckhoven C.;
RT "Linkage and mutation analysis in an extended family with Charcot-
RT Marie-Tooth disease type 1B.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
[7]
RP REVIEW ON CMT1B VARIANTS.
RX MEDLINE=95282670; PubMed=7762451;
RA Roa B.B., Lupski J.R.;
RT "Molecular Genetics of Charcot-Marie-Tooth neuropathy.";
RL Adv. Hum. Genet. 22:117-152(1994).
[8]
RP REVIEW ON CMT1B VARIANTS.
RX MEDLINE=94302675; PubMed=7518101;
RA Patel P.I., Lupski J.R.;
RT "Charcot-Marie-Tooth disease: a new paradigm for the mechanism of
RT inherited disease.";
RL Trends Genet. 10:128-133(1994).
[9]
RP REVIEW ON CMT1B AND DSS VARIANTS.
RX MEDLINE=99103460; PubMed=9888385;
```



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RT "Complete amino acid sequence of P0 protein in bovine peripheral
RT nerve myelin."
RL J. Biol. Chem. 262:4208-4214(1987).
CC -|- FUNCTION: Creation of an extracellular membrane face which guides
CC the wrapping process and ultimately compacts adjacent lamellae.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- TISSUE SPECIFICITY: Found only in peripheral nervous system
CC Schwann cells.
CC -|- PTM: N-LINKED GLYCAN IS SULFATED.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -|- SIMILARITY: Belongs to the myelin P0 protein family.
CC
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CC
CC EMBL; M62860; AAA39867.1; -.
CC EMBL; M62857; AAA39867.1; JOINED.
CC EMBL; M62858; AAA39867.1; JOINED.
CC EMBL; M62859; AAA39867.1; JOINED.
CC HSSP; P06907; INEU.
CC SMART; SM00406; IGV; 1.
CC MGD; MGI:103177; Mpz.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC InterPro; IPR000920; Myelin_P0.
CC PRINTS; PR00213; MYELINP0.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC PROSITE; PS50568; MYELIN P0; 1.
CC Myelin; Structural protein; Glycoprotein; Transmembrane;
CC Phosphorylation; Immunoglobulin domain; Signal.
CC SIGNAL 1 29
CC CHAIN 30 248
CC DOMAIN 30 153
CC TRANSMEM 154 179
CC DOMAIN 180 248
CC DOMAIN 30 143
CC FT DOMAIN 50 127
CC FT DISULFID 122 122
CC FT CARBOHYD 248 AA; 27631 MW; 936D6684300CAC9 CRC64;
SQ
Query Match 6.3%; Score 131; DB 1; Length 248;
Best Local Similarity 25.4%; Pred. No. 0.0014;
Matches 45; Conservative 32; Mismatches 80; Indels 20; Gaps 6;
QY 124 SQVFKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTE-VKHVTKVWEVIFSGRRAKEIV 182
DB 21 SLVLSPALAIVVYTD--REIYGAVGSQVTLHCSFWSSEWSDDISFTWRYQPEGGRDAIS 78
QY 183 FRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMQGVRESGNGNYTCSIHLGNLV 242
DB 79 IFHYAK--GQPYIDEVGAFAKRIQWGDPRWKDGSIVHNLDYSDNGFTTCDVKNPPDI 135
QY 243 FKKT--IVLHVSPEPRTLVTPAALRPLVGNQNLVIGVIVCATILLPLVILIVK 297
DB 136 VKTTSQVTLVPEKVPTRY-----GVVLGA-----VIGGILGVVLLLLLYLIR 180
RESULT 13
MYPO_MOUSE STANDARD; PRT; 248 AA.
AC P06907;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
DE protein) (MPP).
GN MPZ OR P0.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85124601; PubMed=2578885;
RA Lemke G., Axel R.;
RT "Isolation and sequence of a cDNA encoding the major structural
RL protein of peripheral myelin.";
RL Cell 40:501-508(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90166482; PubMed=2483091;
RA Lemke G., Lamar E., Patterson J.;
RT "Isolation and analysis of the gene encoding peripheral myelin
RL protein zero.";
RL Neuron 1:73-83(1988).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 30-148.
RX MEDLINE=96413553; PubMed=8816707;
RA Shapiro L., Doyle J.P., Hensley P., Colman D.R., Hendrickson W.A.;
RT "Crystal structure of the extracellular domain from P0, the major
RL structural protein of peripheral nerve myelin.";
RL Neuron 17:435-449(1996).
CC -!- FUNCTION: Creation of an extracellular membrane face which guides
CC the wrapping process and ultimately compacts adjacent lamellae.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Found only in peripheral nervous system
CC Schwann cells.
CC -!- PTM: N-LINKED GLYCAN IS SULFATED.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Belongs to the myelin P0 protein family.
CC -----
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CC -----
DR EMBL; K03242; AAA41576.1; -
DR PIR; JQ0622; MPRT0.
DR FDB; INEU; 15-MAY-97.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR InterPro; IPR000920; Myelin_P0.
DR PRINTS; PR00213; MYELINP0.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00568; MYELIN P0; 1.
KW Myelin; Structural protein; Glycoprotein; Transmembrane;
KW Phosphorylation; Immunoglobulin domain; Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 248 MYELIN P0 PROTEIN.
FT DOMAIN 30 153 EXTRACELLULAR.
FT TRANSMEM 154 179
FT DOMAIN 180 248
FT DOMAIN 30 143 CYTOPLASMIC.
FT DISULFID 50 127 IG-LIKE V-TYPE.
FT CARBOHYD 122 122 N-LINKED (GLCNAC... ) (COMPLEX).
FT CONFLICT 43 43 G -> R (IN REF. 1).
FT STRAND 31 33
FT STRAND 37 41
FT TURN 42 43
FT TURN 46 48
FT STRAND 51 53
FT STRAND 63 70
FT TURN 71 72
FT STRAND 77 83
FT TURN 84 85
FT TURN 86 89
FT TURN 94 97
FT STRAND 99 101
FT STRAND 104 104

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FT HELIX 105 107
FT TURN 108 108
FT STRAND 109 109
FT STRAND 112 114
FT HELIX 119 121
FT STRAND 123 130
FT STRAND 138 147
SQ SEQUENCE 248 AA; 27570 MW; BB703F173466119B CRC64;

Query Match 6.3%; Score 130; DB 1; Length 248;
Best Local Similarity 25.1%; Pred. No. 0.0016;
Matches 43; Conservative 32; Mismatches 74; Indels 22; Gaps 6;

QY 130 AVLVHLPEEPKELMVHVGGLIQGCVQSTQTE-VKHVTKWEIFSGRAKEEIVFRYTHK 188
DB 29 AIVVYT-----DREYVGAVGVSQVTLHCFSFWSSEWSDDISFTWRYQPEGRDAISIFHYAK 84

QY 189 LRMSVEYSQSWGHFQNRVNLVDIFRNDGSTMQLQVRESGNGNTCSHLGNLVFKKT-- 246
DB 85 ---GQPYIDEVGTGKERIQWVGDPGSKDGSIVHNLDSYDNGTFTCDVKNPDPDIWGKTSQ 141

QY 247 IVLHVSPEEPRTLTPAALRPLVLGNGNLVIVGIVCATILLFVLIIIVK 297
DB 142 VTLVFEKVPTRY-----GWLGA-----VIGGILGVLILLLLFYLR 180

RESULT 14
A33_HUMAN
ID A33_HUMAN STANDARD; PRT; 319 AA.
AC Q99795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cell surface A33 antigen precursor (Glycoprotein A33).
GN GPA33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97165045; PubMed=9012807;
RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA Burgess A.W.;
RT "The human A33 antigen is a transmembrane glycoprotein and a novel
RT member of the immunoglobulin superfamily."
RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
RN [2]
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=97396159; PubMed=9245713;
RA Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA Simpson R.J.;
RT "Characterization of posttranslational modifications of human A33
RT antigen, a novel palmitoylated surface glycoprotein of human
RL gastrointestinal epithelium."
RL Biochem. Biophys. Res. Commun. 236:682-686(1997).
CC -!- FUNCTION: May play a role in cell-cell recognition and signaling.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC epithelium and in 95% of colon cancers.
CC -!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
CC CARBOHYDRATE.
CC -!- PTM: Palmitoylated.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

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DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR004077; IL1_receptor1ip.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00047; IG; 3.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO1539; INTRLEUKINR2.
DR PRINTS; PRO1537; INTRLEUKINR1P.
DR SMART; SM00409; IG; 2.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS00835; IG-LIKE; 3.
DR PROSITE; PS0104; TIR; 1.
KW Receptor; Repeat; Signal; Transmembrane; Immunoglobulin domain;
KW Glycoprotein.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 686 X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY
FT PROTEIN-LIKE 2.
FT DOMAIN 17 354 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 355 375 POTENTIAL.
FT DOMAIN 376 686 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 18 132 IG-LIKE C2-TYPE 1.
FT DOMAIN 141 232 IG-LIKE C2-TYPE 2.
FT DOMAIN 239 347 IG-LIKE C2-TYPE 3.
FT DOMAIN 400 559 TIR.
FT DISULFID 53 116 POTENTIAL.
FT DISULFID 162 214 POTENTIAL.
FT DISULFID 265 331 POTENTIAL.
FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 328 328 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 686 AA; 78669 MW; E400F7ECD186957C CRC64;

Query Match 6.2%; Score 128; DB 1; Length 686;
Best Local Similarity 20.3%; Pred. No. 0.0091;
Matches 80; Conservative 60; Mismatches 135; Indels 120; Gaps 19;

QY 25 VSPPELTVHVGDSALMGCVFQSTEDKCFK-----IDWTLS-----PGEHAKDEYV 70
Db 1 MKPPELL-----ALVCSVSTNLKQVSKNSVDGCDISVDLKYTMALAGEPVVRKA 54

QY 71 LYY-----YS---NLSVPIGRFQNRVHLMGDILCN-----DGSLLLDQVQADQGT 114
Db 55 LFYSVIRTNYSTAQSTGLRLMWYKNKGDLPEPIFSEVRMSKEEDSIWFHSAEQDSGFY 114

QY 115 ICEIRLKGESQVFKAVVHLVLPPEPKELMVHVGGLIOMGCVFQS-----TEVKHVTKEV 170
Db 115 TCVLRL--NSTYCMKVSMSLTVAENE-----SGLCYNSRIRYLEKSEVTKRKE 159

QY 171 I-----FSGRRAKEETVPRYYHKLKRMVSVEYSQSGHFQNRVNLVGDIFENDGSIMLOG 223
Db 160 ISCPDMDDFKSDQEPDVVWYKECKPM-----WRSI-----IIOGNALLIQE 203

QY 224 VRESGGNYTCSIHLGNIVFKKTVILVHVSPEEPTLVTPAALRPLVLGNQLVII----- 278
Db 204 VQEEEDGGNYTCELKVEGKLVRRRTTELKVT-----ALLTDKPKPLFPWENQPSVIDVQLG 258

QY 279 --VGIVCATILL-----PVL-----ILIVKTCGNKSSVNSTVL 311
Db 259 KPLNIPCKAFFGSGSGPMIYMKGEKFI BELAGHIREGIRLKEHLGK-EVELALI 317

QY 312 VKNTKNTNPEIKPCEPCEGEGEKHIYSPILVRE 346
Db 318 FDSV--VEADLANYTCHVENRNGRKH--ASVLLRK 348
```

Search completed: October 1, 2004, 21:04:38
Job time : 29 secs

Blank

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 1, 2004, 20:58:27 ; Search time 119 Seconds
(without alignments)

1044.657 Million cell updates/sec

Title: US-09-989-728-422

Perfect score: 2067

Sequence: 1 MFCPLKLLLPVLDYSLGL.....RNNLEKKSGGMPKTOQAF 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2067	100.0	394	4 Q86YT9	Q86YT9 homo sapien
2	1985	96.0	384	4 Q8N917	Q8N917 homo sapien
3	1783	86.3	394	4 Q7Z499	Q7Z499 homo sapien
4	1364	66.0	283	4 Q8NF70	Q8NF70 homo sapien
5	982	47.5	379	11 Q80JL9	Q80JL9 mus musculus
6	198	9.6	335	13 Q9YGV5	Q9YGV5 gallus gall
7	192	9.3	335	13 Q9PWR4	Q9PWR4 gallus gall
8	191	9.2	335	13 Q9YGH1	Q9YGH1 gallus gall
9	183	8.9	365	6 Q8WMV3	Q8WMV3 bos taurus
10	168	8.1	344	4 Q9UKV4	Q9UKV4 homo sapien
11	167	8.1	2828	4 Q8NR99	Q8NR99 homo sapien
12	164	7.9	319	6 Q9TU80	Q9TU80 canis fami
13	158	7.6	373	4 Q9H6B4	Q9H6B4 homo sapien
14	154.5	7.5	373	11 Q920S5	Q920S5 mus musculus
15	152.5	7.4	372	11 Q8K1G0	Q8K1G0 rattus norv
16	152	7.4	319	6 Q9TU79	Q9TU79 sus scrofa

17	151.5	7.3	437	13 Q90WI4	Q90WI4 gallus gall
18	151	7.3	372	13 Q90Y50	Q90Y50 brachydanio
19	150.5	7.3	373	11 Q8R373	Q8R373 mus musculu
20	147.5	7.1	243	4 Q9UEL4	Q9UEL4 homo sapien
21	147.5	7.1	269	4 Q95297	Q95297 homo sapien
22	147	7.1	330	11 P97269	P97269 cavia porce
23	147	7.1	344	11 Q9R067	Q9R067 rattus norv
24	147	7.1	358	11 Q9R066	Q9R066 rattus norv
25	147	7.1	584	4 Q9Y3X8	Q9Y3X8 homo sapien
26	146	7.1	352	11 Q91W66	Q91W66 mus musculu
27	146	7.1	365	11 Q9DBJ8	Q9DBJ8 mus musculu
28	144.5	7.0	183	4 Q9UEL6	Q9UEL6 homo sapien
29	144.5	7.0	209	4 Q9NYK4	Q9NYK4 homo sapien
30	142.5	6.9	202	4 Q8IX11	Q8IX11 homo sapien
31	142	6.9	337	11 P97268	P97268 cavia porce
32	140	6.8	215	11 Q91WI4	Q91WI4 mus musculu
33	139.5	6.7	329	13 Q9IAY6	Q9IAY6 spherooides
34	138.5	6.7	318	13 Q91664	Q91664 xenopus lae
35	137.5	6.7	907	5 Q9NEGO	Q9NEGO drosophila
36	137.5	6.7	3215	5 Q8IRV7	Q8IRV7 drosophila
37	137.5	6.7	4117	5 Q8IRV9	Q8IRV9 drosophila
38	137.5	6.7	4179	5 Q9W4Y4	Q9W4Y4 drosophila
39	137.5	6.7	4223	5 Q8MPN3	Q8MPN3 drosophila
40	137.5	6.7	4228	5 Q8IRV8	Q8IRV8 drosophila
41	136	6.6	338	4 Q8IV49	Q8IV49 homo sapien
42	136	6.6	339	13 Q9IAZ1	Q9IAZ1 spherooides
43	135.5	6.6	199	13 Q8UG36	Q8UG36 brachydanio
44	134.5	6.5	403	6 Q9N2H5	Q9N2H5 equus cabal
45	134	6.5	252	4 Q8WWT6	Q8WWT6 homo sapien

ALIGNMENTS

RESULT 1

Q86YT9 ID Q86YT9 PRELIMINARY; PRT; 394 AA.
AC Q86YT9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adhesion molecule AMICA.
GN AMICA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Foster J.S., Gurney A.L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY138965; AAN52117.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 394 AA; 44339 MW; 64B542F9384C7642 CRC64;

Query Match 100.0%; Score 2067; DB 4; Length 394;

Best Local Similarity 100.0%; Pred. No. 3.1e-181;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFCPLKLLLPVLDYSLGLNDLVNSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLs 60

Db 1 MFCPLKLLLPVLDYSLGLNDLVNSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLs 60

Qy 61 PGEHAKDEYVLYYNSLVSPVIGRFQNVHLMGDIILCNDGSLILQDVQADQGTTCIRL 120

Db 61 PGEHAKDEYVLYYNSLVSPVIGRFQNVHLMGDIILCNDGSLILQDVQADQGTTCIRL 120

Qy 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLTQMCVCFQSTEVKHVTKEVTFSGRRAKEE 180

Db 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLTQMCVCFQSTEVKHVTKEVTFSGRRAKEE 180

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QY 181 IVFYYHKLKMSVYSQSGHGFQNRVNLVGDIFRNDGSLMVGVSQSGNVTCSIHLCN 240
|||||
Db 181 IVFYYHKLKMSVYSQSGHGFQNRVNLVGDIFRNDGSLMVGVSQSGNVTCSIHLCN 240
|||||

QY 241 LVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIVGIVCATILLPVLLIVKKT 300
|||||
Db 241 LVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIVGIVCATILLPVLLIVKKT 300
|||||

QY 301 GNKSVNSTVLVNTKKNPEIKKPCFPERCEGKHYSPIIIVREVIEEPEPSKSRAT 360
|||||
Db 301 GNKSVNSTVLVNTKKNPEIKKPCFPERCEGKHYSPIIIVREVIEEPEPSKSRAT 360
|||||

QY 361 YMTMPVPSLRSRDRNLSLEKSGGMPKTOQAF 394
|||||
Db 361 YMTMPVPSLRSRDRNLSLEKSGGMPKTOQAF 394
|||||

RESULT 2
Q8N917
ID Q8N917 PRELIMINARY; PRT; 384 AA.
AC Q8N917;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ37080.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK094399; BAC04347.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 384 AA; 43091 MW; C93D8EF6C97E6591 CRC64;

Query Match 96.0%; Score 1985; DB 4; Length 384;
Best Local Similarity 99.5%; Pred. No. 1e-173;
Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 DYSGLNDLNSPPELTIVHVGDSALMGCVFQSTEDKCFIKIDWTLSPGSHAKDEVLYYY 74
|||||
Db 5 DYSGLNDLNSPPELTIVHVGDSALMGCVFQSTEDKCFIKIDWTLSPGSHAKDEVLYYY 64
|||||

QY 75 SNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQDQGTTCYCEIRLKGESQVFKXAVLIH 134
|||||
Db 65 SNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQDQGTTCYCEIRLKGESQVFKXAVLIH 124
|||||

QY 135 VLPEEPKELMHVHGLIQMGCVFQSTEVKHTVKEWIFSGRAKEEIVFRRYHKLMSVE 194
|||||
Db 125 VLPEEPKELMHVHGLIQMGCVFQSTEVKHTVKEWIFSGRAKEEIVFRRYHKLMSAE 184
|||||

QY 195 YSQSGHGFQNRVNLVGDIFRNDGSLMVGVSQSGNVTCSIHLCNVLVFKKTIIVLHVSPE 254
|||||
Db 185 YSQSGHGFQNRVNLVGDIFRNDGSLMVGVSQSGNVTCSIHLCNVLVFKKTIIVLHVSPE 244
|||||

QY 255 EPTLVTPAALRPLVLGGNQLVIVGIVCATILLPVLLIVKKTGKNSVNSTVLVKN 314
|||||
```

```
Db 245 EPTLVTPAALRPLVLGGNQLVIVGIVCATILLPVLLIVKKTGKNSVNSTVLVKN 304
|||||
QY 315 TKKTNPEIKKPCFPERCEGKHYSPIIIVREVIEEPEPSKSEATYMTMHPVPSLRS 374
|||||
Db 305 TKKTNPEIKKPCFPERCEGKHYSPIIIVREVIEEPEPSKSEATYMTMHPVPSLRS 364
|||||

QY 375 RNSLEKSGGMPKTOQAF 394
|||||
Db 365 RNSLEKSGGMPKTOQAF 384
|||||

RESULT 3
Q7Z499
ID Q7Z499 PRELIMINARY; PRT; 394 AA.
AC Q7Z499;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Putative junctional adhesion molecule precursor.
GN JAML.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Moog-Lutz C., Cave-Riant F., Guibal F.C., Breau M., Di Gioia Y.,
RA Cayre Y.E., Lutz P.G.;
RT "JAML, a novel protein induced in myeloid leukemia cells, has
RT characteristics of a junctional adhesion molecule.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ15553; CAD56620.1; -.
KW Signal.
FT SIGNAL.
FT CHAIN 1 19 Potential.
SQ SEQUENCE 394 AA; 43731 MW; B81F99C929D80C53 CRC64;

Query Match 86.3%; Score 1783; DB 4; Length 394;
Best Local Similarity 87.0%; Pred. No. 3.7e-155;
Matches 354; Conservative 7; Mismatches 20; Indels 26; Gaps 4;

QY 1 MFCPLKLLPVLLDYSGLNDLNSPPELTIVHVGDSALMGCVFQSTEDKCFIKIDWTLS 60
|||||
Db 1 MFCPLKLLPVLLDYSGLNDLNSPPELTIVHVGDSALMGCVFQSTEDKCFIKIDWTLS 60
|||||

QY 61 PGEHAKDEVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQDQGTTCYCEIRL 120
|||||
Db 61 PGEHAKDEVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQDQGTTCYCEIRL 120
|||||

QY 121 KGESQVFKKAVLVHLPPEPKELMHVHGLIQMGCVFQSTEVKHTVKEWIFSGRAKEE 180
|||||
Db 121 KGESQVFKKAVLVHLPPEPKELMHVHGLIQMGCVFQSTQ-----DGAQ-RRR 168
|||||

QY 181 IVF-----RYHHKMSVEYSQSGHGFQNRVNLVGDIFRNDGSLMVGVS 227
|||||
Db 169 LVFVTTTNSGCLRSFPRAGATSRIGSE-TRQGRMDIFNLVGDIFRNDGSLMVGVS 227
|||||

QY 228 DGGNYTCSIHLCNVLVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIVGIVCATIL 287
|||||
Db 228 DGGNYTCSIHLCNVLVFKKTIIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIVGIVCATIL 287
|||||

QY 288 LLPVLILVKKTCGKNSVNSTVLVNTKKNPEIKKPCFPERCEGKHYSPIIIVREV 347
|||||
Db 288 LLPVLILVKKTCGKNSVNSTVLVNTKKNPEIKKPCFPERCEGKHYSPIIIVREV 347
|||||

QY 348 IEIEEPEPSKSEATYMTMHPVPSLRSRDRNLSLEKSGGMPKTOQAF 394
|||||
Db 348 IEIEEPEPSKSEATYMTMHPVPSLRSRDRNLSLEKSGGMPKTOQAF 394
|||||

RESULT 4
Q8NF70
```

```

ID Q8NF70 PRELIMINARY; PRT; 283 AA.
AC Q8NF70;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FLJ00300 protein (Fragment).
GN FLJ00300.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RT spleen."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090409; BAC03390.1; -.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON TER 1
SQ SEQUENCE 283 AA; 32079 MW; CCACB5B0839EB30E CRC64;

Query Match 66.0%; Score 1364; DB 4; Length 283;
Best Local Similarity 99.2%; Pred. No. 7.3e-117;
Matches 257; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCPLKLLPVLDDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIFKIDWTL 60
DB 25 MFCPLKLLPVLDDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIFKIDWTL 84
QY 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDLICNDGSLLLQDVQADQGTICIRL 120
DB 85 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDLICNDGSLLLQDVQADQGTICIRL 144
QY 121 KGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHTKVEMIFSGRAKEE 180
DB 145 KGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHTKVEMIFSGRAKEE 204
QY 181 IVFRRYHKLMSVEYSQSGHGFQNRVNLVGDIFRNDGSIIMLQGVRESDGGNVTCSIH 240
DB 205 IVFRRYHKLMSVEYSQSGHGFQNRVNLVGDIFRNDGSIIMLQGVRESDGGNVTCSIH 264
QY 241 LVFKKTIHLVSPPEPTL 259
DB 265 LVFKKTIHLVSPPEPTL 283

RESULT 5
ID Q8OUL9 PRELIMINARY; PRT; 379 AA.
AC Q8OUL9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to adhesion molecule AMICA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B5/EGFP transgenic ICR mice; TISSUE=Trophoblast Stem Cell;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC050133; AAH0133.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR003596; Ig_v.

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DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGc2; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 379 AA; 42561 MW; 2CC0F2987CB12B7F CRC64;

Query Match 47.5%; Score 982; DB 11; Length 379;
Best Local Similarity 56.1%; Pred. No. 1.3e-81;
Matches 222; Conservative 35; Mismatches 105; Indels 34; Gaps 9;

QY 1 MFCPLKLLPVLVLL---DYSGLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCIFKIDW 57
DB 1 MLCLLKLLIPIVILAPVGPQGLPLTVSSPOLRVHVGESVLMGCVVQRTTEKHVDVDM 60
QY 58 TLSPGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDLICNDGSLLLQDVQADQGTICICE 117
DB 61 LFSKDKDDASEYVLYYNSLVSVPTGRFQNRSHLVGDTFHNDSGLLLQDVQKADGEIYTC 120
QY 118 IRLGESQVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFQSTEVKHTKVEMIF-SGRR 176
DB 121 IRLKNSVMWKKPVLELWLPPEPKDLRVVGDITQMRCSIQSTEEKRVTKVNMWPFSSGSH 180
QY 177 AKBEIVFRYYHKLMSVEYSQSGHGFQNRVNLVGDIFRNDGSIIMLQGVRESDGGNVTCSI 236
DB 181 TEEETVLSYDSNMRSG--KFQSLGRFRNRVDLTGDISRNDGSIKLTVKESDRGIYTCI 238
QY 237 HLGNLVFKKTIHLVSPPEPTLVTPAALRPL-----VLGGNQLVIIVGVICATILLP 290
DB 239 YVGLKESRKTIVLVHVGDEFQRTISPT--PTDKGQQGILNGNQLVIIVGVICATILLP 296
QY 291 VLLIIVKTKCGKSSVNSTVLVK--NTKKNPEIKPKCHFERCEGEKHIYSPILVREV 347
DB 297 VLLIIVKAKWKS SVSSMASVKSLENKEKINP-----EKHIYSITTWET 342
QY 348 IEEPESEKSEATYMTMHPVMPSLRSRDNNSLEKKS 383
DB 343 TERGISGE-SEGTYMTWNPVWFS--SPKASSLVRS 375

RESULT 6
QYGV5 PRELIMINARY; PRT; 335 AA.
ID QYGV5
AC QYGV5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cht1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95077161; PubMed=9862345;
RA Chretien I., Marcuz A., Courtet M., Kateruo K., Vainio O., Heath J.K.,
RA White S.J., Du Pasquier L.;
RT "CTX, a Xenopus thymocyte receptor, defines a molecular family
RT conserved throughout vertebrates."
RL Eur. J. Immunol. 28:4094-4104(1998).
DR EMBL; AF061023; AAD17523.1; -.
DR HSPD; P06907; INEU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 335 AA; 36561 MW; 071A313C3CE6DCA0 CRC64;

Query Match 9.6%; Score 198; DB 13; Length 335;
Best Local Similarity 22.1%; Pred. No. 1.2e-09;
Matches 88; Conservative 74; Mismatches 158; Indels 78; Gaps 17;

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QY 1 MFCKLILLPVLLDYSGLNDLNVSPPELTVHV--GDSALMGCVFQSTEDKCIKIDWT 58
DB 1 MF-PTMLKIFPILATLAGHVRGVVTVPEKTVNVTGNGNATLLCTYTSSQPLGNFFIQWS 59
QY 59 LSPGSHAKDEVLYYYNSLSPVIGRQNRVHLMGDIILCNDGSLLLQDVQADQGTIYCEI 118
DB 60 FYSAKESQLHTIYYSEGQSYSGEFKORI--TAATSPGNASITISNMQPSDTGTYCEV 117
QY 119 RL----KGESQVFKAVVLHVL--PEEP---KELMHVHGLIOMGCVFQSTEVKHTVKE 169
DB 118 FSPQDADQSQ---KSVIVNVLVKPSKPFCKIEGTPEKGHLIYLKCKDQ--GLSHTP--- 170
QY 170 WIFSRRAKEETVFRYYHKLMSVYSQSWGHGFQNRVNLVGDIFRNDGSLMLQ--VRES 228
DB 171 -----YAWY-----KVD-----ENTLPTVTEYFNPDTGILYIGNLTTFE 204
QY 229 GGNVTCSTHGLNLFVKTKTIVLHVSPEEPTLTVPAALRPLVLGGNQLVIIIGVIVCATILL 288
DB 205 TGHYRCI--ASNIMGSTCELDLTSMHSDGNIVAGAL-----IGAILAAVII 249
QY 289 LPVLLIVKTKCGNKSSVNTVLKNTKTNPEIKPKCHPERCEGKHIYSPPIIVREVI 348
DB 250 CAIVWVLTKAKKKSSNE--MQVMAQKQNAEYAVP-----NEENTPQAVLPNSA 301
QY 349 EEEPSKSEATYTMHPWPSLRSDRNSLEKSGGG 386
DB 302 TNEQPSADEAASETP-----ENDEKHEVQKEETAG 332

RESULT 7

Q9PWR4
ID Q9PWR4 PRELIMINARY; PRT; 335 AA.
AC Q9PWR4
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Chrl thymocyte antigen precursor.
GN Chrl.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H.B19; TISSUE=Thymus;
RA Katelyu K.H., Boyd R., Gobel T.T., Bean A., Dunon D., Imhof B.A.,
RA Vainio O.;
RT "Chrl, a new Igsf member inhibits thymocyte differentiation at the
RT double positive stage.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y14064; CAA74391.1; -.
DR HSSP; P06907; INEU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 335 CHrl THYMOCYTE ANTIGEN.
SQ SEQUENCE 335 AA; 36509 MW; AA6159598079B438 CRC64;

Query Match 9.3%; Score 192; DB 13; Length 335;
Best Local Similarity 22.1%; Pred. No. 4.1e-09;
Matches 88; Conservative 76; Mismatches 156; Indels 78; Gaps 18;

QY 1 MFCKLILLPVLLDYSGLNDLNVSPPELTVHV--GDSALMGCVFQSTEDKCIKIDWT 58
DB 1 MF-PTMLKIFPILATLAGHVRGVVTVPEKTVNVTGNGNATLLCTYTSSQPLGNFFIQWS 59
QY 59 LSPGSHAKDEVLYYYNSLSPVIGRQNRVHLMGDIILCNDGSLLLQDVQADQGTIYCEI 118

DB 60 FYSAKESQLHTIYYSEGQSYSGEFKORI--TAATSPGNASITISNMQPSDTGTYCEV 117
DB 118 FSPQDADQSQ---KSVIVNVLVKPSKPFCKIEGTPEKGHLIYLKCKDQ--GLPHTP--- 170
QY 170 WIFSRRAKEETVFRYYHKLMSVYSQSWGHGFQNRVNLVGDIFRNDGSLMLQ--VRES 228
DB 171 -----YAWY-----KVD-----ENTLPTVTEYFNPDTGILYIGNLTTFE 204
QY 229 GGNVTCSTHGLNLFVKTKTIVLHVSPEEPTLTVPAALRPLVLGGNQLVIIIGVIVCATILL 288
DB 205 TGHYRCI--ASNIMGSTCELDLTSMHSDGNIVAGAL-----IGAILAAVII 249
QY 289 LPVLLIVKTKCGNKSSVNTVLKNTKTNPEIKPKCHPERCEGKHIYSPPIIVREVI 348
DB 250 CAIVWVLTKAKKKSSNE--MQVMAQKQNAEYAVP-----NEENTPQAVLPNSA 301
QY 349 EEEPSKSEATYTMHPWPSLRSDRNSLEKSGGG 386
DB 302 TNEQPSADEAAA-----PETP-----ENDEKHEVQKEETAG 332

RESULT 8

Q9YGH1
ID Q9YGH1 PRELIMINARY; PRT; 335 AA.
AC Q9YGH1
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Chrl thymocyte antigen precursor.
GN Chrl.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RPRL line 0; TISSUE=Thymus;
RA Katelyu K.H., Boyd R., Gobel T.T., Bean A., Dunon D., Imhof B.A.,
RA Vainio O.;
RT "Chrl, a new Igsf member inhibits thymocyte differentiation at the
RT double positive stage.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y14063; CAA74390.1; -.
DR HSSP; P06907; INEU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 335 CHrl THYMOCYTE ANTIGEN.
SQ SEQUENCE 335 AA; 36553 MW; AA640C5CD02CB16D CRC64;

Query Match 9.2%; Score 191; DB 13; Length 335;
Best Local Similarity 22.1%; Pred. No. 5.1e-09;
Matches 88; Conservative 76; Mismatches 156; Indels 78; Gaps 18;

QY 1 MFCKLILLPVLLDYSGLNDLNVSPPELTVHV--GDSALMGCVFQSTEDKCIKIDWT 58
DB 1 MF-PTMLKIFPILATLAGHVRGVVTVPEKTVNVTGNGNATLLCTYTSSQPLGNFFIQWS 59
QY 59 LSPGSHAKDEVLYYYNSLSPVIGRQNRVHLMGDIILCNDGSLLLQDVQADQGTIYCEI 118
DB 60 FYSAKESQLHTIYYSEGQSYSGEFKORI--TAATSPGNASITISNMQPSDTGTYCEV 117
QY 119 RL----KGESQVFKAVVLHVL--PEEP---KELMHVHGLIOMGCVFQSTEVKHTVKE 169
DB 118 FSPQDADQSQ---KSVIVNVLVKPSKPFCKIEGTPEKGHLIYLKCKDQ--GLPHTP--- 170

Db 283 PPKSRTSTARSY-----IGSNHSLGMSPSNMEGYSKTQ 317

RESULT 11

Q9NR99 PRELIMINARY; PRT; 2828 AA.
AC Q9NR99
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Adican.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Placenta;
RA Crowl R.M., Luk D.;
RT "Identification of the gene encoding Adican, a novel protein
expressed in human arthritic tissues.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF245505; AAF86402.1; -.
DR HSP; P56276; 1TLK.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR Pfam; PF00047; IG; 12.
DR Pfam; PF00560; LRR; 6.
DR Pfam; PF01463; LRRCT; 1.
DR SMART; SM00408; IGc2; 10.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRCT; 1.
DR SMART; SM00369; LRR_TYP; 3.
DR PROSITE; PS00835; IG LIKE; 12.
KW Immunoglobulin domain
SQ SEQUENCE 2828 AA; 312291 MW; A18377D8554F1PE1 CRC64;

Query Match 8.1%; Score 167; DB 4; Length 2828;
Best Local Similarity 21.8%; Pred. No. 1.5e-05;
Matches 87; Conservative 74; Mismatches 149; Indels 90; Gaps 20;

Qy 42 CVFQST--EDKCFKIDWTLSG--EHAQD-EYVLYYSNI-----SVP 80
Db 2221 CVARNKVGDDYVLLKVDVWMPKPAKIEHKEENDHKVFYGGDLKVDCAVATGLPNPEISWSLP 2280
Qy 81 IGRFQNRVHLMGD-----ILCNDGSLLLQDVOEADQGYIC--EIRL-KGDSQVFK 129
Db 2281 DGSIVNSFMQSDSGGRTKRYVFNNGTLFVNGVMEEGDYTCFAENQVGKDMRVVK 2340
Qy 130 AVLVHLPPEPKELMHV--GGLIQMGCVFQSTEVKHVTVKVEWIFSGRRAKEEIVFRYH 187
Db 2341 VVTAPATIRNKTVLAVQVYGVVVTVAC---EAKGEPMPKVWLSPTNKV----- 2387
Qy 188 KLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLGVSDDGNYTCSIHGLNLFVKTI 247
Db 2388 -IPTSEKYQIY-----ODGTLIQAQRSDSGNYTCLVNSAGEDKRTV 2431
Qy 248 VLHVSPEEPTLVTP---AALRPVLGNGQNLVI---IVGIVCATIL-LLPVLILVKKTC 300
Db 2432 WIHVNQPPKINGPNPITVREIAAGSRKLDCKAEGITPRVLWAFEGVVLPAFY 2491
Qy 301 GNKSSV--NSTVLVKNTKTNPEIKPKCHFERCEGKHIYSPIIVREVIEE---EEP-S 354
Db 2492 GNRITVHGNGSLDIRSKS--DSVQLVCMARNEGGEARLIVQLTVLEPKEPIFDHPIS 2549
Qy 355 EKSEATVMTWHPV-----WPSLRSDRNNLSLEKKS 384
Db 2550 EK--ITAMAGHTISLNCSAAGTPTPSLWVWLPNGTDLQSG 2587

RESULT 12

Q9TU80 PRELIMINARY; PRT; 319 AA.
AC Q9TU80
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Coxsackie-adenovirus-receptor homolog (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed German shepherd; TISSUE=Liver;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtemuller A.B., Schultheiss H.-P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does
not correlate with adenovector targeting in vivo indicating anatomical
vector barriers.";
RL Gene Ther. 6:1520-1535(1999).
DR EMBL; AF109645; AAF01256.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS00835; IG LIKE; 2.
KW Immunoglobulin domain; Receptor.
FT NON TER 319
SQ SEQUENCE 319 AA; 35422 MW; 85C63A6EC7986965 CRC64;

Query Match 7.9%; Score 164; DB 6; Length 319;
Best Local Similarity 22.6%; Pred. No. 1.4e-06;
Matches 91; Conservative 61; Mismatches 146; Indels 104; Gaps 19;

Qy 5 LKILLPVLDYSLGNDLNVSPPELVH--VGDLSALMGCVFQ-STEDKCFKIDWTLS 61
Db 5 LRFVLLCGVADFT---RSLSIITPEQMIKAKGETAYLPCKFTLSPEQGLDIEWLLSP 61
Qy 62 GEHAKDEYVLYYSNLSVPICRFQ---RVHL-MGDLICNDGSLLLQDVOEADQGYICE 117
Db 62 ADNQKVDQVILYSGDKIYDDYTDQLKGRVHFTSNLKGSDASINVTNRLSDIGTYQCK 121
Qy 118 IRLKGBSQVFKKAVLVHLPPEPKELMHVHVGGLIQMGCVF---QSTEVKHVTVKVEWIFS 173
Db 122 V--KXAPGVGNKKIQLTVL--VKPSGIRCYVDGSEIENDPKLCEPKESGLPLQYEW--- 175
Qy 174 GRRAKEEIVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLGVSDDGNYT 233
Db 176 -----QKLSNSQKTPPSWS-----TDMTSPV-----ISIKNASTEYSCTYI 211
Qy 234 CSHLGNLVFKKTVILHVSPE--EPRTLVTPAALRPLVLGNGQNLVIIVGIVCATILLPV 291
Db 212 C-----TVTNRVSDQCQLRLNVVPPSNRAGTIAG---AVVG-----ILLALV 251
Qy 292 LILIVKTKCGNKSVMNSTVLVKNTKTNPEIKPKCHFERCEGKHIYSPIIVREVIEE 351
Db 252 LIGFIVPCC-----RKKREKYEKEVHHD-----IRE 280
Qy 352 EPSEKSEATVMTWHPWPSLRSDRNN--SLEKSGGGMPKTK 391
Db 281 VPPLKSRSTARSY-----IGSNHSLGMSPSNMEGYSKTQ 317

RESULT 13

Q9H6B4 PRELIMINARY; PRT; 373 AA.
ID Q9H6B4
AC Q9H6B4

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLU22415 (Adipocyte-specific adhesion
DE molecule).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Oiyashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Eguchi J., Wada J., Hida K., Zhang H.;
RL "Molecular cloning of adipocyte-specific adhesion molecule (ASAM).";
DR EMBL; AK026068; BAB15347.1; -.
DR EMBL; BC009371; AAH09371.1; -.
DR EMBL; AY326422; AAP88386.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 373 AA; 41280 MW; FDA215EB3B3C4335 CRC64;

Query Match          7.6%; Score 158; DB 4; Length 373;
Best Local Similarity 20.8%; Pred. No. 6.4e-06;
Matches 84; Conservative 73; Mismatches 132; Indels 114; Gaps 20;

QY 5 LKLLLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFO-STEDKCFKIDWTLSPGE 63
DB 1 MSLLLLLVSYVGTGLGHT---EIKRVAEKVTLPHCHQLGLPEKDTLDIEWLLTNE 57
QY 64 HAKDEYVLY----YYSNLSVPIGRFQNRVHLMGDI LCNDSGLLDQVQADQGTTCYICIR 119
DB 58 GNQKVVIITYSSRRHYNNLT---EEQGRVAFASFLAGDASLIQIEPLKPSDEGRYTCVK 114
QY 120 LKGE---SOVFKKAVLVHLPPEPK---ELMVHVGGLIQMGCVFOSTEVKHTVKVEMIFS 173
DB 115 NSGRYVNSHVILKVL---VRSPKPCKELEGELTEGSDTLQCESS----- 157
QY 174 GRRAKEEIVFRRYHKLMSVEYSQSWGHFQ-----NRVNLVGDIFRNDGSI MLQGVRES 228
DB 158 ---GTEPIVY-YWQRIK-----EKEGEDERLPKPSRID-----YNHFGVLLQNTMSY 202
QY 229 GGVTCSTHLGNLVFKKTIIVLHVSPEEPRTLVPAALRPLVLGNQLVIVGIVCATILL 288
DB 203 SGLYQCT--AGNEAGKESCVVRVTQVYQSI-----GMVAGA-----VTGIVAGALLI 248
QY 289 LPVLILVKKTCGNKSSVNSTVLVNTKTNPEIKKPCHEKPCERCEGKHYSPIIVREVI 348
DB 249 FLLVWLLIR-----KDK-----ERYE----- 265
QY 349 EEEFPE-KSATYMTMHPVWPSLRSDRNNLSLEKSGGGMPT 390
DB 266 EEEERNEIREDAEPKARLVKPS--SSSGSRSSRSRSGSSTES 306

RESULT 14
Q920S5
ID Q920S5 PRELIMINARY; PRT; 373 AA.
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AC Q920S5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adipocyte-specific protein 5.
GN 9030425E11RIK OR ASP5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsuruga H.;
RT "Adipocyte-specific protein 5, a novel protein upregulated during
RT adipocyte differentiation.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040490; BAB68503.1; -.
DR MGD; MGI:1918816; 9030425E11RIK.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 373 AA; 41186 MW; 5C6280584AF95326 CRC64;

Query Match          7.5%; Score 154.5; DB 11; Length 373;
Best Local Similarity 21.2%; Pred. No. 1.3e-05;
Matches 77; Conservative 61; Mismatches 116; Indels 109; Gaps 18;

QY 49 DKCIFKIDWTLSPGEHAKDEYVLY----YYSNLSVPIGRFQNRVHLMGDI LCNDSGLLDQ 104
DB 42 EKDTLDIEWLLTDNEGNQKVVIITYSSRRHYNNLT---EEQGRVAFASFLAGDASLIQIE 98
QY 105 DVQADQGTTCYICIRLKE---SOVFKKAVLVHLPPEPKELMVHVGGLIQMGCVFOS-- 159
DB 99 PLKPSDEGRYTCVKNSGRYVNSHVILKAL---VRSPKPK-----CELEGE 142
QY 160 TEVXHTVKVWFIFGRRAKEEIVFRRYHKLMSVEYSQSWGHF--QNRVNLVGDIFRNDG 217
DB 143 TEGSDTLTQCESASGK---PIVY-YWQRIK-----EKEGEDERLPKPSRID-----YNNPG 190
QY 218 SIMLQGVRESGGNYTCSIHLGNLVFKKTIIVLHVSPEEPRTLVPAALRPLVLGNQLVI 277
DB 191 RVLLQNTLMASGGYQCT--AGNEAGKESCVVRVTQVYQSI-----GMVAGA----- 236
QY 278 IVGVICATILLPVLILVKKTCGNKSSVNSTVLVNTKTNPEIKKPCHEKPCERCEGKH 337
DB 237 VTGIVAGALLIFLLIWL-----LIRKSKDRIYEEEDRP----- 269
QY 338 IYSPILVREVEIEEB-----PSEKSEATYMTMHPVWPSLRSDRNNLSLEKSGGGMPT 389
DB 270 -----NEIREDAEPKARLVKPSSSSGS-----RSSRSGSSSTRSTGNSAS 311
QY 390 TQQ 392
DB 312 RSQ 314

RESULT 15
Q8K1G0
ID Q8K1G0 PRELIMINARY; PRT; 372 AA.
AC Q8K1G0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Visceral adipose tissue-specific transmembrane protein Ol-16.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
```

RC STRAIN=OLETF; TISSUE=Visceral adipose;
 RA Hida K., Wada J., Zhang H., Makino H.;
 RT "Molecular cloning of visceral adipose tissue-specific gene."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF302047; AAM76974.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_C2.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain; Transmembrane.

SEQUENCE 372 AA; 41148 MW; 439AB3C4D3E56346 CRC64;

Query Match	7.4%	Score 152.5;	DB 11;	Length 372;
Best Local Similarity	21.9%	Pred. No. 2e-05;		
Matches	79;	Conservative	61;	Mismatches 116; Indels 105; Gaps 19;

QY	49	KCIPKIDWTLSPGEHAKDEYVLY----	YYSNLSPDGRFQNRVHLMGDI	CNDGSLLLQ	104
DB	42	EKDTLDIEWLLTDNEGQKQVITYSSRHVYNNLT---	EEQKGRVAFASNFLAGDASLQIE	98	
QY	105	DVQEADQGTyceIRLKEB--SQVFKKAVLHLVLP	PEPKELMVHVGGLIQMGCVFQS--	159	
DB	99	PLKPSDEGRYTCVKNRGVYVWSHVILKVL----	VRPSKP-----CELEGE	142	
QY	160	TEVKHVTKEVIFSGRRAKEEIVFRTYHKLMSVEYSQSWGHF--	QNRVNLVGDIFRNDG	217	
DB	143	TEGSDTLTQCESASGTK--PIVY-YWQRIR--	EKEGEDEHLPPKSRID----	YNNPG	190
QY	218	SIMLQGVRESGNGNTCSIHNLNLFVKKTIVLHVSPPEPRTLVT	PAALRPLVLGGNQLVI	277	
DB	191	RVLLQNLTMASGLYQCT--AGNEAKESCVVRVTQVYQSI--	-----GMVAGA-----	236	
QY	278	IVGIVCATILLAPLILIVKTKCGNKSSVNSVLVKNTKTNPEIK	KEKPCFCEGEKH	337	
DB	237	VTGIVAGALLIFLLIWLILR-----	-----KSK-----ERYE-----	264	
QY	338	IYSPIIVREVIEEPEPSE-KSEATYMTMHPVWPS-----	LRSDRNNSLEKSGGGMPTQ	391	
DB	265	-----BEDRPNEIREDAEAPRARLVKPSSSSSSGSRSSRSGSS	STRSTGNSASRS	313	
QY	392	Q 392			
DB	314	Q 314			

Search completed: October 1, 2004, 21:06:47
 Job time : 127 secs